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OM protein - protein search, using sw model

Run on: October 12, 2004, 15:46:05 ; Search time 54 Seconds  
(without alignments)  
1465.061 Million cell updates/sec

Title: US-09-807-148-9

Perfect score: 1553

Sequence: 1 GFGTKKXVHFVFNKGNVLI.....BEDKEEDBEDVPCQAKDEL 280

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- A Genesep 29Jan04:\*
- 1: Genesep1980s:\*
  - 2: Genesep1990s:\*
  - 3: Genesep2000s:\*
  - 4: Genesep2001s:\*
  - 5: Genesep2002s:\*
  - 6: Genesep2003as:\*
  - 7: Genesep2003bs:\*
  - 8: Genesep2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1553	100.0	280	3	AA92355
2	1553	100.0	400	3	AA92355 Recombina
3	1553	100.0	417	1	AA92350
4	1553	100.0	417	1	AA92276 60 kD Ro
5	1553	100.0	417	2	AA900927
6	1553	100.0	417	3	AA92349 Human MBP
7	1553	100.0	417	5	AAU77712 Human cal
8	1553	100.0	417	5	AAE24591 Human cal
9	1553	100.0	417	5	AAE18851 Human cal
10	1553	100.0	417	5	AB822384 Human cal
11	1553	100.0	417	6	ABJ19766 Human MP2
12	1553	100.0	417	6	AA979824 Calreticu
13	1553	100.0	417	7	AD22407 HLA-B46 T
14	1553	100.0	417	7	AD56308 Human pro
15	1553	100.0	417	7	AD56312 Human pro
16	1476.5	95.1	416	7	AD56306 Rat Prote
17	1476.5	95.1	416	7	AD56310 Rat Prote
18	1442.5	92.9	401	2	AAW11156
19	1031.5	66.4	406	4	AB64414 Drosophil
20	1022.5	65.8	403	2	AAW04171 Flea calr
21	935.5	62.0	336	2	AAI2312 Partial s
22	856.5	55.2	415	4	AA56343 Castor be
23	856.5	55.2	415	4	AA56341 Castor be
24	837.5	53.9	420	5	AB504556 Maize cal
25	823	53.0	312	3	AA924609 Arabidops

26	823	53.0	421	3	AA924608
27	823	53.0	424	3	AA924607
28	816	52.5	312	3	AA947933
29	816	52.5	421	3	AA947932
30	816	52.5	424	3	AA947931
31	812	52.3	419	7	ABM74155
32	801.5	51.6	332	3	AA930998
33	801.5	51.6	441	3	AA930997
34	801.5	51.6	444	3	AA930986
35	715	46.0	428	7	AAW74288
36	702	45.2	122	2	AA900924
37	699	45.0	122	2	AA900926
38	678	43.7	122	2	AA900925
39	633	40.8	591	4	AB844553
40	629	40.5	591	7	AB85248 Rat calne
41	629	40.5	591	7	AD611368
42	628	40.5	591	7	AD611376
43	628	40.5	591	7	AD611380
44	629	40.5	591	7	AD611372
45	629	40.5	591	7	AD660129
					AA924608 Arabidops
					AA924607 Arabidops
					AA947933 Arabidops
					AA947932 Arabidops
					AA947931 Arabidops
					ABM74155 DNA clone
					AA930998 Arabidops
					AA930997 Arabidops
					AA930986 Arabidops
					AAW74288 DNA clone
					AA900924 Human ccl
					AA900926 Rat cclqr
					AA900925 Mouse ccl
					AB844553 Mouse wou
					AB85248 Rat calne
					AD611368 Rat Prote
					AD611376 Rat Prote
					AD611380 Rat Prote
					AD611372 Rat Prote
					AD660129 Rat Prote

## ALIGNMENTS

### RESULT 1

AA92355  
ID RAY92355 standard; protein; 280 AA.

XX  
AC RAY92355;

XX  
DT 10-AUG-2000 (first entry)

XX  
DE Recombinant delta-120 calreticulin.

XX  
KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;

XX  
KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;

XX  
KW cytotatic; dermalogical; immunosuppressive; antiinflammatory; hepatic;

XX  
KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.

XX  
OS Homo sapiens.

XX  
OS Synthetic.

XX  
PN WC200020577-A1.

XX  
PD 13-APR-2000.

XX  
PF 05-OCT-1999; 99WO-US023240.

XX  
PR 06-OCT-1998; 98US-0103438P.

XX  
PA (USSH ) US-DEPT HEALTH & HUMAN SERVICES.

XX  
PI Tosato G, Pike SE, Yao L;

XX  
DR WPI; 2000-303767/26.

XX  
PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,

XX  
PT useful for suppressing tumor growth.

XX  
PS Claim 4; Page 86; 99pp; English.

XX  
CC This sequence comprises recombinant human calreticulin (AA92355) missing the N-terminal 120 amino acids. A novel method of inhibiting endothelial cell growth comprises contacting the cells with calreticulin (or its fragments/variants). Fragments of calreticulin causes at least 40% inhibition of angiogenesis, tumor growth and/or endothelial cell growth (claimed). The method may be used for inhibiting angiogenesis in a patient. The angiogenesis is associated with a disease other than a tumor that is associated with neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia, trachoma, neovascular glaucoma, psoriasis, angiodermas, immune inflammation, atherosclerosis, excessive wound repair, retinal neovascularization, macular degeneration, corneal graft



PT DNA sequences encoding antigenic epitope(s) of RO 60 KD auto-antigen -  
PT used in immunoassays to detect rheumatic disease.  
XX Disclosure; Fig 2; 88pp; English.  
PS  
XX  
CC Synthetic peptides corresp. to an epitopic core of Ro antigen are  
CC expressed recombinantly to detect autoantibodies, for identification of  
CC autoimmune diseases. These epitopes are Aas 24-36, 23-36, 188-209, or 241  
CC -255. The peptides may be substd. for ribonucleoprotein particle  
CC antigens. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-  
CC MAR-2003 to correct PI field.)  
XX Sequence 417 AA;  
SQ  
Query Match 100.0%; Score 1553; DB 1; Length 417;  
Best Local Similarity 100.0%; Pred. No. 4.2e-122;  
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GPGTKVHVIFNYKGNVLINKDIRCKDDEFTLTLIVRPDNTYEVKIDNSQVSGSLE 60  
DB 138 GPGTKVHVIFNYKGNVLINKDIRCKDDEFTLTLIVRPDNTYEVKIDNSQVSGSLE 197  
QY 61 DDWDFLPPKKIKDPDASKPEDWDERAKIDDPDTSKPEDWKPHEIPDPDAKXPEDWDEEM 120  
DB 198 DDWDFLPPKKIKDPDASKPEDWDERAKIDDPDTSKPEDWKPHEIPDPDAKXPEDWDEEM 257  
QY 121 DGEWEPPIQNPYKGEWKPRQIDNPDKGTWHPHPEIDNPESDPDSIYAYDNFVGLGLD 180  
DB 258 DGEWEPPIQNPYKGEWKPRQIDNPDKGTWHPHPEIDNPESDPDSIYAYDNFVGLGLD 317  
QY 181 LMQVKSGTIFDNFLITNDEAYAEFGNETGWTKAAEKQMKDKODEQRLEKEEEDKKRK 240  
DB 318 LMQVKSGTIFDNFLITNDEAYAEFGNETGWTKAAEKQMKDKODEQRLEKEEEDKKRK 377  
RESULT 4  
AA00927  
ID AA00927 standard; protein; 417 AA.  
XX  
AC AA00927;  
XX  
DT 28-MAY-1999 (first entry)  
XX  
DE Calreticulin.  
XX  
KW C1q and collectin receptor; c1qr binding domain; complement ubiquitin;  
KW CUB functionality; inhibitor; complement activation; inflammation;  
KW myocardial infarction; brain ischaemia; gut ischaemia; amyloid plaque;  
KW rheumatoid arthritis; systemic lupus erythematosus; Alzheimer's disease;  
KW immune complex nephritis; therapy.  
XX  
OS Homo sapiens.  
XX  
PN WO9507406-A1.  
XX  
PD 18-FEB-1999.  
XX  
PF 12-AUG-1999; 98WO-GB002430.  
XX  
PR 12-AUG-1997; 97GB-00016998.  
XX  
PA (UYLE-) UNIV LEICESTER.  
XX  
PI Schwaeble W;  
XX  
DR WPI; 1999-180404/15.  
XX  
PT Use of a c1qr binding domain - to modulate complement ubiquitin (CUB)  
PT functionality.

XX Disclosure; Page 26-27; 31pp; English.  
PS  
XX  
CC This sequence is calreticulin, a homologue of C1q and collectin receptor  
CC (c1qr). The invention relates to the use of a c1qr binding domain in a  
CC medicament to effect complement ubiquitin (CUB) functionality, and an  
CC inhibitor of the c1qr binding domain in a medicament to inhibit CUB  
CC functionality. The c1qr binding domain, or its inhibitor, can be used to  
CC treat a human or animal body. Particularly an inhibitor is used to treat  
CC complement activation involved in the initiation and maintenance of  
CC inflammation, for example in myocardial infarction, brain ischaemia  
CC (stroke), gut ischaemia, rheumatoid arthritis, systemic lupus  
CC erythematosus, burns, immune complex nephritis, and to treat amyloid  
CC plaques in Alzheimer's disease. The use of c1qr binding domain or  
CC inhibitor enables the CUB domain functionality to be modulated using a  
CC low molecular weight molecule  
XX  
SQ Sequence 417 AA;  
Query Match 100.0%; Score 1553; DB 2; Length 417;  
Best Local Similarity 100.0%; Pred. No. 4.2e-122;  
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GPGTKVHVIFNYKGNVLINKDIRCKDDEFTLTLIVRPDNTYEVKIDNSQVSGSLE 60  
DB 138 GPGTKVHVIFNYKGNVLINKDIRCKDDEFTLTLIVRPDNTYEVKIDNSQVSGSLE 197  
QY 61 DDWDFLPPKKIKDPDASKPEDWDERAKIDDPDTSKPEDWKPHEIPDPDAKXPEDWDEEM 120  
DB 198 DDWDFLPPKKIKDPDASKPEDWDERAKIDDPDTSKPEDWKPHEIPDPDAKXPEDWDEEM 257  
QY 121 DGEWEPPIQNPYKGEWKPRQIDNPDKGTWHPHPEIDNPESDPDSIYAYDNFVGLGLD 180  
DB 258 DGEWEPPIQNPYKGEWKPRQIDNPDKGTWHPHPEIDNPESDPDSIYAYDNFVGLGLD 317  
QY 181 LMQVKSGTIFDNFLITNDEAYAEFGNETGWTKAAEKQMKDKODEQRLEKEEEDKKRK 240  
DB 318 LMQVKSGTIFDNFLITNDEAYAEFGNETGWTKAAEKQMKDKODEQRLEKEEEDKKRK 377  
RESULT 5  
AA92349  
ID AA92349 standard; protein; 417 AA.  
XX  
AC AA92349;  
XX  
DT 10-AUG-2000 (first entry)  
XX  
DE Human MBP-calreticulin.  
XX  
KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;  
KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;  
KW cyrostatic; dermatological; immunosuppressive; antiinflammatory; hepatic;  
KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.  
XX  
OS Homo sapiens.  
XX  
PH Key Location/Qualifiers  
FT Peptide 1..17  
FT Protein /label= signal\_peptide  
FT Protein 18  
FT Protein /label= mature\_protein  
XX  
PN WO200020577-A1.  
XX  
PD 13-APR-2000.  
XX  
PF 05-OCT-1999; 99WO-US023240.  
XX

PR 06-OCT-1998; 98US-0103438P.  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Tosato G, Pike SE, Yao L;  
 XX  
 DR WPI; 2000-303767/26.  
 DR N-PSDB; AAA09346, AAA09347.  
 XX  
 XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,  
 PT useful for suppressing tumor growth.  
 XX  
 PS Disclosure; Page 79-80; 99pp; English.  
 XX  
 CC A novel method of inhibiting endothelial cell growth comprises contacting  
 CC the cells with calreticulin (or its fragments/variants). Fragments of  
 CC calreticulin causes at least 40% inhibition of angiogenesis, tumor growth  
 CC and/or endothelial cell growth (claimed). The method may be used for  
 CC inhibiting angiogenesis in a patient. The angiogenesis is associated with  
 CC a disease other than a tumor that is associated with neovascularization  
 CC (e.g. diabetic neuropathy, retrolental fibroplasia, trachoma, neovascular  
 CC glaucoma, psoriasis, angiofibromas, immune inflammation,  
 CC atherosclerosis, excessive wound repair, retinal neovascularization,  
 CC macular degeneration, corneal graft rejection, contact lens overwear,  
 CC Crohn's disease, non-immune inflammation, rheumatoid arthritis, systemic  
 CC lupus erythematosus, thyroiditis, Goodpasture's syndrome, systemic  
 CC vasculitis, scleroderma, Sjorgen's syndrome, sarcoidosis and primary  
 CC biliary cirrhosis). The method may also be used for treating/inhibiting  
 CC tumor growth especially Kaposi's sarcoma (claimed)  
 XX  
 SQ Sequence 417 AA;  
 Query Match 100.0%; Score 1553; DB 3; Length 417;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-122;  
 Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GPGTKKVHVIENYKGNVLINKDKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSLE 60  
 DB 138 GPGTKKVHVIENYKGNVLINKDKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSLE 197  
 QY 61 DDWDFLPPKKIKDPDASKPEDWDERAKIDDPDTSKPEDWDPKPEHIPDPDAKPEDWDEEM 120  
 DB 198 DDWDFLPPKKIKDPDASKPEDWDERAKIDDPDTSKPEDWDPKPEHIPDPDAKPEDWDEEM 257  
 QY 121 DGEWEPPIQNPYKGEWKPRQIDNPYKGTWTHPEIDNPYSPDPSIYADNFGVLGLD 180  
 DB 258 DGEWEPPIQNPYKGEWKPRQIDNPYKGTWTHPEIDNPYSPDPSIYADNFGVLGLD 317  
 QY 181 LMQVKSGTIFDNFLITNDEAYAEFGNETWGTVAEKQMKDKQDEBQRLKEEEDKKRK 240  
 DB 318 LMQVKSGTIFDNFLITNDEAYAEFGNETWGTVAEKQMKDKQDEBQRLKEEEDKKRK 377  
 QY 241 EEEAEKDEDDKDEDEEEDKEEEDVPGQAKDEL 280  
 DB 378 EEEAEKDEDDKDEDEEEDKEEEDVPGQAKDEL 417  
 RESULT 6  
 AAU77712  
 ID AAU77712 standard; protein; 417 AA.  
 XX  
 AC AAU77712;  
 XX  
 DT 05-JUN-2002 (first entry)  
 XX  
 DE Human calreticulin (CRT).  
 XX  
 KW Calreticulin; CRT; endoplasmic reticulum chaperone polypeptide;  
 KW cytosolic; vaccine; human papillomavirus 16; HPV 16; E7; DNA vaccine;  
 KW enhanced antigen-specific immune response; cytotoxic T lymphocyte;  
 KW tumour; cancer; cervical cancer.  
 XX  
 OS Homo sapiens.

XX WC200212281-A2.  
 PN  
 XX  
 PD 14-FEB-2002.  
 XX  
 XX 02-AUG-2001; 2001WO-US024134.  
 XX PF  
 XX 03-AUG-2000; 2000US-0222902P.  
 XX PR  
 XX (UYJO ) UNIV JOHNS HOPKINS.  
 PA  
 PI Wu T, Hung C;  
 XX  
 XX WPI; 2002-257463/30.  
 DR N-PSDB; ABK11662.  
 XX  
 PT New nucleic acids encoding a fusion polypeptide comprising an endoplasmic  
 PT reticulum chaperone polypeptide linked to an antigenic polypeptide,  
 PT useful as a vaccine for inducing antigen-specific immune responses.  
 XX  
 PS Disclosure; Page 27; 71pp; English.  
 XX  
 CC The invention describes a nucleic acid molecule (I) encoding a fusion  
 CC polypeptide comprising a first polypeptide domain comprising an  
 CC endoplasmic reticulum chaperone polypeptide e.g. calreticulin (CRT) and a  
 CC second polypeptide domain comprising at least one antigenic peptide e.g.  
 CC human papillomavirus 16 (HPV 16) E7. The nucleic acid is useful as a  
 CC vaccine (DNA vaccine) for inducing enhanced antigen-specific immune  
 CC responses, particularly those mediated by cytotoxic T lymphocytes. The  
 CC nucleic acid and compositions comprising the nucleic acid is also useful  
 CC for inhibiting the growth of tumours and cancers e.g. cervical cancer.  
 CC This is the amino acid sequence of the human calreticulin (CRT), an  
 CC endoplasmic reticulum protein used in the creation of a DNA vaccine  
 XX  
 SQ Sequence 417 AA;  
 Query Match 100.0%; Score 1553; DB 5; Length 417;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-122;  
 Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GPGTKKVHVIENYKGNVLINKDKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSLE 60  
 DB 138 GPGTKKVHVIENYKGNVLINKDKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSLE 197  
 QY 61 DDWDFLPPKKIKDPDASKPEDWDERAKIDDPDTSKPEDWDPKPEHIPDPDAKPEDWDEEM 120  
 DB 198 DDWDFLPPKKIKDPDASKPEDWDERAKIDDPDTSKPEDWDPKPEHIPDPDAKPEDWDEEM 257  
 QY 121 DGEWEPPIQNPYKGEWKPRQIDNPYKGTWTHPEIDNPYSPDPSIYADNFGVLGLD 180  
 DB 258 DGEWEPPIQNPYKGEWKPRQIDNPYKGTWTHPEIDNPYSPDPSIYADNFGVLGLD 317  
 QY 181 LMQVKSGTIFDNFLITNDEAYAEFGNETWGTVAEKQMKDKQDEBQRLKEEEDKKRK 240  
 DB 318 LMQVKSGTIFDNFLITNDEAYAEFGNETWGTVAEKQMKDKQDEBQRLKEEEDKKRK 377  
 QY 241 EEEAEKDEDDKDEDEEEDKEEEDVPGQAKDEL 280  
 DB 378 EEEAEKDEDDKDEDEEEDKEEEDVPGQAKDEL 417  
 RESULT 7  
 AAU24591  
 ID AAU24591 standard; protein; 417 AA.  
 XX  
 AC AAU24591;  
 XX  
 DT 04-OCT-2002 (first entry)  
 XX  
 DE Human calreticulin protein.  
 XX  
 KW Human; calreticulin; antisense compound; hyperproliferative disorder;  
 KW cancer; autoimmune disease; viral infection; cardiovascular disease;





CC diagnosis, therapy and pharmaceutical development. The modulators are  
CC useful in a variety of diagnostic and therapeutic applications including  
CC angiogenic, apoptotic and cell proliferation disorders. This sequence  
CC represents an MP21 protein of the invention  
XX  
SQ Sequence 417 AA;  
  
Query Match 100.0%; Score 1553; DB 6; Length 417;  
Best Local Similarity 100.0%; Pred. No. 4.2e-122;  
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 GPGTKKVVHVIYNYKGNVLINIKDKDETHLYTLIVRPDNTYEVKIDNSQVSGSLE 60  
Db 138 GPGTKKVVHVIYNYKGNVLINIKDKDETHLYTLIVRPDNTYEVKIDNSQVSGSLE 197  
  
Qy 61 DDWDFLPPKKIKDPDASKPEDWDERAKIDDDTDSKPEDWDPKPEHIPDPDAKKPEDWDEEM 120  
Db 198 DDWDFLPPKKIKDPDASKPEDWDERAKIDDDTDSKPEDWDPKPEHIPDPDAKKPEDWDEEM 257  
  
Qy 121 DGEWPEPPVIQNPYKGEWKPRQIDNPDKYGTWHPHPEIDNPESYSPDPSIYAYDNFVGLGLD 180  
Db 258 DGEWPEPPVIQNPYKGEWKPRQIDNPDKYGTWHPHPEIDNPESYSPDPSIYAYDNFVGLGLD 317  
  
Qy 181 LWQVKSGTIFDNFLITNDAYAEFGNETGWVTKAAEKQMKQKQDEEQLKEEEDKKRK 240  
Db 318 LWQVKSGTIFDNFLITNDAYAEFGNETGWVTKAAEKQMKQKQDEEQLKEEEDKKRK 377  
  
Qy 241 EEEAEKDEDDKDEDEEDKDEEEDKDEEEDVPGQAKDEL 280  
Db 378 EEEAEKDEDDKDEDEEDKDEEEDKDEEEDVPGQAKDEL 417  
  
RESULT 11  
ID AAG79824 standard; protein; 417 AA.  
XX  
AC AAG79824;  
XX  
DT 16-APR-2003 (first entry)  
XX  
DE Calreticulin.  
XX  
KW Motif: SE; signal transduction; Alzheimer's disease; neuronal cell;  
KW calreticulin; arrhythmia; idiopathic nephritic syndrome;  
KW non-autoimmune hyperthyroidism; obesity; polycystic kidney disease;  
KW cancer; asthma; atopic dermatitis; psoriasis; rheumatoid arthritis;  
KW systemic lupus erythematosus; infectious disease; atherosclerosis;  
KW inflammatory bowel disease; osteoarthritis; septic shock;  
KW congestive heart failure; insulin-resistance syndrome;  
KW ischaemia-reperfusion injury.  
XX  
OS Homo sapiens.  
XX  
FN WO200299061-A2.  
XX  
PD 12-DEC-2002.  
XX  
PF 04-JUN-2002; 2002WO-US017536.  
XX  
PR 04-JUN-2001; 2001US-0295691P.  
XX  
PR 03-JUN-2002; 2002US-00161959.  
XX  
PA (UNWI ) UNIV MICHIGAN.  
XX  
PI Holoshitz J, Ling S;  
XX  
DR WPI; 2003-156953/15.  
XX  
PT Treating diseases associated with signal transduction aberrations, e.g.  
PT Alzheimer's disease, arrhythmia or rheumatoid arthritis, comprises  
PT administering a preparation comprising an SE- or an SE motif-containing  
PT peptide.  
XX

PS Disclosure; Fig 14; 97pp; English.  
XX  
CC This sequence represents human calreticulin. This protein was used in the  
CC method of the invention for treating diseases associated with signal  
CC transduction aberrations. The method comprises: (a) providing a subject  
CC with one or more symptoms of Alzheimer's disease and, optionally, a  
CC plurality of neuronal cells expressing calreticulin, and a preparation  
CC comprising an shared epitope (SE) - containing peptide or a peptide which  
CC binds the calreticulin; and (b) administering the preparation to the  
CC subject. The inventive method is useful for treating diseases associated  
CC with signal transduction aberrations, such as Alzheimer's disease,  
CC arrhythmia, idiopathic nephritic syndrome, non-autoimmune  
CC hyperthyroidism, obesity, polycystic kidney disease, cancer, asthma,  
CC atopic dermatitis, psoriasis, rheumatoid arthritis, systemic lupus  
CC erythematosus, infectious diseases, inflammatory bowel disease,  
CC osteoarthritis, septic shock, atherosclerosis, congestive heart failure,  
CC insulin-resistance syndrome, and ischaemia-reperfusion injury  
XX  
SQ Sequence 417 AA;  
  
Query Match 100.0%; Score 1553; DB 6; Length 417;  
Best Local Similarity 100.0%; Pred. No. 4.2e-122;  
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 GPGTKKVVHVIYNYKGNVLINIKDKDETHLYTLIVRPDNTYEVKIDNSQVSGSLE 60  
Db 138 GPGTKKVVHVIYNYKGNVLINIKDKDETHLYTLIVRPDNTYEVKIDNSQVSGSLE 197  
  
Qy 61 DDWDFLPPKKIKDPDASKPEDWDERAKIDDDTDSKPEDWDPKPEHIPDPDAKKPEDWDEEM 120  
Db 198 DDWDFLPPKKIKDPDASKPEDWDERAKIDDDTDSKPEDWDPKPEHIPDPDAKKPEDWDEEM 257  
  
Qy 121 DGEWPEPPVIQNPYKGEWKPRQIDNPDKYGTWHPHPEIDNPESYSPDPSIYAYDNFVGLGLD 180  
Db 258 DGEWPEPPVIQNPYKGEWKPRQIDNPDKYGTWHPHPEIDNPESYSPDPSIYAYDNFVGLGLD 317  
  
Qy 181 LWQVKSGTIFDNFLITNDAYAEFGNETGWVTKAAEKQMKQKQDEEQLKEEEDKKRK 240  
Db 318 LWQVKSGTIFDNFLITNDAYAEFGNETGWVTKAAEKQMKQKQDEEQLKEEEDKKRK 377  
  
Qy 241 EEEAEKDEDDKDEDEEDKDEEEDKDEEEDVPGQAKDEL 280  
Db 378 EEEAEKDEDDKDEDEEDKDEEEDKDEEEDVPGQAKDEL 417  
  
RESULT 12  
ID ADA26337 standard; protein; 417 AA.  
XX  
AC ADA26337;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Human calreticulin protein SEQ ID NO:14.  
XX  
KW stress response protein; immune response; tumour;  
KW tumour growth inhibition; metastasis; cytostatic; vaccine; gene therapy;  
KW human; calreticulin.  
XX  
OS Homo sapiens.  
XX  
FN WO2003068941-A2.  
XX  
PD 21-AUG-2003.  
XX  
PF 13-FEB-2003; 2003WO-US004631.  
XX  
PR 13-FEB-2002; 2002US-0356293P.  
XX  
PA (UYDU-) UNIV DUKE.  
XX  
PI Nicchita C, Baker-Lepain J;  
XX

DR WPI; 2003-679635/64.  
 DR N-PSDB; ADA26336.  
 XX  
 PT New Hsp60, Hsp70, Hsp90 or calreticulin polypeptide, useful for preparing  
 PT a composition for inhibiting tumor growth or metastasis in a subject.  
 XX  
 PS Disclosure; Page 137-138; 150pp; English.  
 XX  
 CC The present invention describes a recombinant stress response polypeptide  
 CC (I) free of an antigen-binding domain, where the recombinant stress  
 CC response polypeptide comprises an extracellularly transported polypeptide  
 CC when expressed in a host cell. Also described: (1) a composition for  
 CC eliciting an immune response in a subject; (2) eliciting an immune  
 CC response in a subject; and (3) inhibiting tumour growth or metastasis in  
 CC a subject. (I) has cytostatic activity, and can be used in vaccines and  
 CC in gene therapy. The polypeptide (I) can be used for preparing a  
 CC composition for inhibiting tumour growth or metastasis in a subject. The  
 CC present sequence represents human calreticulin, which is a stress  
 CC response polypeptide given in the exemplification of the present  
 CC invention.  
 XX  
 SQ Sequence 417 AA;  
 Query Match 100.0%; Score 1553; DB 6; Length 417;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-122;  
 Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GPGTKKHVIFNYKGNVLINKIRCKDDETHLYTLIVRPDNTYEVKIDNSQVESGSL 60  
 DB 138 GFGTKKHVIFNYKGNVLINKIRCKDDETHLYTLIVRPDNTYEVKIDNSQVESGSL 197  
 QY 61 DDWDFLPFKIKDPDASKPEDWDERAKIDDDTDSKPEDWDERAKIDDPDPAKPEDWDEEM 120  
 DB 198 DDWDFLPFKIKDPDASKPEDWDERAKIDDDTDSKPEDWDERAKIDDPDPAKPEDWDEEM 257  
 QY 121 DGEWPPVQNPYKGEWKPRQIDNPDKYKGTWIIHPEIDNPYSPPDSIYAYDNFVGLGLD 180  
 DB 258 DGEWPPVQNPYKGEWKPRQIDNPDKYKGTWIIHPEIDNPYSPPDSIYAYDNFVGLGLD 317  
 QY 181 LMQVKSGTIFNFLTNDDEAYAEFGNETGWTKAAEKQMKDKODEBQRLKEEEDKKRK 240  
 DB 318 LMQVKSGTIFNFLTNDDEAYAEFGNETGWTKAAEKQMKDKODEBQRLKEEEDKKRK 377  
 QY 241 EEEAEADKEDDEDDEDEEDKEEEDVPGQAKDEL 280  
 DB 378 EEEAEADKEDDEDDEDEEDKEEEDVPGQAKDEL 417  
 RESULT 13  
 ADD22407  
 ID ADD22407 standard; protein; 417 AA.  
 XX  
 AC ADD22407;  
 XX  
 DT 15-JAN-2004 (first entry)  
 XX  
 DE HLA-B46 T cell recognised tumour antigenic polypeptide, SEQ No 57.  
 XX  
 KW tumour antigenic peptide; cancer; vaccine; cytostatic; cytotoxic T cell;  
 KW colon; mouth; lung; prostatic; gynecological; human.  
 XX  
 OS Homo sapiens.  
 XX  
 FN JP2003111595-A.  
 XX  
 PD 15-APR-2003.  
 XX  
 PF 24-JUN-2002; 2002JP-00183603.  
 XX  
 PR 25-JUN-2001; 2001JP-00191974.  
 XX  
 FA (ITCY/) ITO Y.  
 XX

DR WPI; 2003-611129/58.  
 XX  
 PT Novel tumor antigenic peptide or polypeptide useful for inducing  
 PT cytotoxic T cells or for treating cancer such as colon, mouth, lung,  
 PT prostatic or gynecological cancer.  
 XX  
 PS Claim 2; SEQ ID NO 57; 98pp; Japanese.  
 XX  
 CC The invention relates to a novel tumour antigenic peptide or polypeptide  
 CC comprising a sequence selected from 99 sequences fully defined in the  
 CC specification. The tumour antigenic peptide or polypeptide comprises a  
 CC sequence selected from 99 sequences fully defined in the specification,  
 CC where the tumour antigenic peptide preferably has a sequence of Glu-Pro-  
 CC pro-Leu-Ser-Gln-Glu-Thr-Phe, and the polypeptide preferably has a  
 CC sequence comprising 393 amino acids fully defined in the specification.  
 CC The invention further provides a cancer vaccine comprising a tumour  
 CC antigenic peptide or polypeptide, which has cytostatic activity. A tumour  
 CC antigenic peptide, polypeptide, its encoding polynucleotide, a  
 CC hybridising polynucleotide, a recombinant vector containing the  
 CC polynucleotide, a host transformed with the vector or an antibody are  
 CC useful for screening for compounds that interact with the tumour  
 CC antigenic peptide, the polypeptide or its encoding polynucleotide and  
 CC increases the expression of the tumour antigenic peptide, the polypeptide  
 CC or polynucleotide. The tumour antigenic peptide or the polypeptide is  
 CC useful for inducing cytotoxic T cells. The tumour antigenic peptide  
 CC vaccine is useful for treating cancer such as colon, mouth, lung,  
 CC prostatic or gynecological cancer. The invention also provides a  
 CC pharmaceutical composition useful for treating cancer. The tumour  
 CC antigenic peptide or the polypeptide is useful as an antigen to create  
 CC antibodies. This sequence represents one of the tumour antigenic  
 CC polypeptides of the invention.  
 XX  
 SQ Sequence 417 AA;  
 Query Match 100.0%; Score 1553; DB 7; Length 417;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-122;  
 Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GPGTKKHVIFNYKGNVLINKIRCKDDETHLYTLIVRPDNTYEVKIDNSQVESGSL 60  
 DB 138 GFGTKKHVIFNYKGNVLINKIRCKDDETHLYTLIVRPDNTYEVKIDNSQVESGSL 197  
 QY 61 DDWDFLPFKIKDPDASKPEDWDERAKIDDDTDSKPEDWDERAKIDDPDPAKPEDWDEEM 120  
 DB 198 DDWDFLPFKIKDPDASKPEDWDERAKIDDDTDSKPEDWDERAKIDDPDPAKPEDWDEEM 257  
 QY 121 DGEWPPVQNPYKGEWKPRQIDNPDKYKGTWIIHPEIDNPYSPPDSIYAYDNFVGLGLD 180  
 DB 258 DGEWPPVQNPYKGEWKPRQIDNPDKYKGTWIIHPEIDNPYSPPDSIYAYDNFVGLGLD 317  
 QY 181 LMQVKSGTIFNFLTNDDEAYAEFGNETGWTKAAEKQMKDKODEBQRLKEEEDKKRK 240  
 DB 318 LMQVKSGTIFNFLTNDDEAYAEFGNETGWTKAAEKQMKDKODEBQRLKEEEDKKRK 377  
 QY 241 EEEAEADKEDDEDDEDEEDKEEEDVPGQAKDEL 280  
 DB 378 EEEAEADKEDDEDDEDEEDKEEEDVPGQAKDEL 417  
 RESULT 14  
 ADE56308  
 ID ADE56308 standard; protein; 417 AA.  
 XX  
 AC ADE56308;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE Human Protein NP\_004334, SEQ ID NO 2160.  
 XX  
 KW Human; pain; neuronal tissue; gene therapy;  
 KW spinal segmental nerve injury; chronic constriction injury; CCI;  
 KW spared nerve injury; SNI; Chung.  
 XX



**Dd**      318 INQVKSGTIFDNFLINTDEAYAEFGNETWGVTKAAEKMKDKQDEQRLEKEEDKKKXK 377  
  
 **QY**         241 EEEEAADKDDDEDKDDEDEDEKDEEDEDVPQAQDEL 280  
                |||||  
**Dd**         378 EEEAEEKDDEDKDDEDEDEKDEEDEDVPQAQDEL 417  
                |||||  
  
RESULT 15  
ADES6312 standard; protein; 417 AA.  
XX AC ADE56312;  
XX DT 29-JAN-2004 (first entry)  
XX DE Human Protein NP\_004334, SEQ ID NO 2164.  
DE XX  
KW Human; pain; neuronal tissue; gene therapy;  
KM spinal segmental nerve injury; Chronic constriction injury; CCI;  
KW spared nerve injury; SNI; Chung.  
XX OS Homo sapiens.  
OS XX WO2003016475-A2.  
PN XX  
XX PD 27-FEB-2003.  
XX PF 14-AUG-2002; 2002WO-USO25765.  
XX PR 14-AUG-2001; 2001US-0312147P.  
PR PR 01-NOV-2001; 2001US-0346382P.  
XX PR 26-NOV-2001; 2001US-0333347P.  
XX PA (GEMO ) GEN HOSPITAL CORP.  
PA (FARS ) BAYER AG.  
XX W Woolf C, D'urso D, Befort K, Costigan M;  
PI WPI; 2003-268312/26.  
DR GENBANK; NP\_004334.  
XX PT New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.  
XX PS Claim 1; Page; 1017pp; English.

The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published pct sequences.

OS	Homo sapiens.
XX	WO2003016475-A2.
PN	
XX	27-FEB-2003.
PD	
XX	14-AUG-2002; 2002WO-US025765.
PF	
XX	14-AUG-2001; 2001US-0312147P.
XX	01-NOV-2001; 2001US-0346382P.
PR	
XX	26-NOV-2001; 2001US-0333347P.
XX	(GEO ) GEN HOSPITAL CORP.
PA	(FARB ) BAYER AG.
XX	
PI	Woolf C, D'urso D, Befort K, Costigan M;
PI	WPI: 2003-268312/26.
DR	GENEANK, NP_004334.
DR	
XX	New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
PFT	
PPT	Claim 1; Page; 101pp; English.
XX	
CC	The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX	
SQ	Sequence 417 AA;
	Query Watch
	Best Local Similarity 100.0%; Score 1553; DB 7; Length 417;
	Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY	1 GPGETKKVHVFNYKGNVLINLIRCKDDETHLYTLIVRPDNTYEVKIDNSOVESGSLE 60
DB	138 GPGETKKVHVFNYKGNVLINLIRCKDDETHLYTLIVRPDNTYEVKIDNSOVESGSLE 197
QY	61 DDWDLFPPKKIKDPDASKPEDWDERAKIDDPTDSKPEDWKPEHIPDDPAKKPEDWDEM 120
DB	198 DDWDLFPPKKIKDPDASKPEDWDERAKIDDPTDSKPEDWKPEHIPDDPAKKPEDWDEM 257
QY	121 DGWEPPPVTQNPEYGEWKPKQINDNPDKGTWIHPEIDNPEYSPDSPSIAYDNFGVLGLD 180
DB	258 DGWEPPPVTQNPEYGEWKPKQINDNPDKGTWIHPEIDNPEYSPDSPSIAYDNFGVLGLD 317
QY	181 LQWKSQTIFDNFLITNDSEAAVEEGNETGWTKIAAEKQMKDKODEQRUKKEEEDKKRK 240

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XX
SQ Sequence 417 AA;
Query Match 100.0%; Score 1553; DB 7; Length 417;
Best Local Similarity 100.0%; Pred. No. 4.2e-122;
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPGTKKVVIFNYKGNVLINKDIRCKDDETHLYTLIVRPDNTYEVKIDNSQVSGSLE 60
Db 138 GPGTKKVVIFNYKGNVLINKDIRCKDDETHLYTLIVRPDNTYEVKIDNSQVSGSLE 197
QY 61 DDWDFLPPKKIKDPDASKPEDWDERAKIDDDPTDSKPEDWPKPEHIPDPDAKKPEDWDEEM 120
Db 198 DDWDFLPPKKIKDPDASKPEDWDERAKIDDDPTDSKPEDWPKPEHIPDPDAKKPEDWDEEM 257
QY 121 DGEWEPPIQNPYKGEWKPRQIONPDYKGTWIIHPEIDNPEYSPDPSIYAYDNFVGLGLD 180
Db 258 DGEWEPPIQNPYKGEWKPRQIONPDYKGTWIIHPEIDNPEYSPDPSIYAYDNFVGLGLD 317
QY 181 LWQVKSGTIFNFLTNDDEAYAEFFGNETWGTAAEKQMKDKODEEQRLEKEEEDKKRK 240
Db 318 LWQVKSGTIFNFLTNDDEAYAEFFGNETWGTAAEKQMKDKODEEQRLEKEEEDKKRK 377
QY 241 EEEEAEDKEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 280
Db 378 EEEEAEDKEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 417
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Search completed: October 12, 2004, 15:48:29  
Job time : 56 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 12, 2004, 15:46:06 ; Search time 19 Seconds  
(without alignments)  
760.804 Million cell updates/sec

Title: US-09-807-148-9

Perfect score: 1553

Sequence: 1 GPGTKKHVIFNYKGNVLI.....EEDKEDEBEDVFGQAKDEL 280

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.\*

- 1: /cgn2\_6/ptodata/2/iaa/5A.COMB.pep.\*
- 2: /cgn2\_6/ptodata/2/iaa/5B.COMB.pep.\*
- 3: /cgn2\_6/ptodata/2/iaa/6A.COMB.pep.\*
- 4: /cgn2\_6/ptodata/2/iaa/6B.COMB.pep.\*
- 5: /cgn2\_6/ptodata/2/iaa/PCTUS.COMB.pep.\*
- 6: /cgn2\_6/ptodata/2/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1549	99.7	416	4	US-09-828-000-2
2	856.5	55.2	415	3	US-08-675-816-2
3	624	40.2	593	1	US-08-298-382-2
4	577.5	37.2	610	4	US-09-976-594-947
5	493	31.7	542	3	US-08-675-816-6
6	318	20.5	61	4	US-09-828-000-8
7	318	20.5	180	4	US-09-828-000-3
8	235	15.1	61	4	US-09-828-000-4
9	189	12.2	35	4	US-09-828-000-7
10	184.5	11.9	714	2	US-08-990-114-3
11	184.5	11.9	714	4	US-09-241-333-3
12	184.5	11.9	740	1	US-08-257-073-5
13	175.5	11.3	1162	4	US-08-728-323A-2
14	175.5	11.3	1162	4	US-09-298-568-2
15	175.5	11.3	1162	4	US-09-410-399-2
16	163	10.5	905	2	US-08-574-959A-9
17	163	10.5	905	3	US-09-357-014-9
18	163	10.5	1135	2	US-08-574-959A-7
19	163	10.5	1135	3	US-09-357-014-7
20	151	9.7	740	3	US-09-022-983-5
21	150.5	9.7	546	3	US-08-935-855-20
22	149	9.6	411	2	US-08-741-134-6
23	146	9.4	754	3	US-09-214-564A-2
24	146	9.4	764	4	US-09-370-838-67
25	143.5	9.2	197	4	US-09-486-147-40
26	143.5	9.2	240	4	US-08-114-555A-8
27	143.5	9.2	240	3	US-08-559-397A-14

28	142	9.1	27	4	US-09-828-000-5	Sequence 5, Appli
29	137	8.8	633	1	US-08-458-477A-5	Sequence 5, Appli
30	137	8.8	633	2	US-09-033-153-5	Sequence 5, Appli
31	137	8.8	633	3	US-09-325-430B-5	Sequence 5, Appli
32	137	8.8	765	2	US-08-663-112-2	Sequence 2, Appli
33	135	8.7	295	2	US-08-679-765-5	Sequence 5, Appli
34	135	8.7	295	2	US-09-196-525-5	Sequence 5, Appli
35	135	8.7	295	3	US-09-318-317-5	Sequence 5, Appli
36	135	8.7	295	4	US-09-177-165A-22	Sequence 22, Appli
37	134.5	8.7	231	3	US-09-461-697-194	Sequence 194, App
38	134.5	8.7	232	3	US-09-461-697-192	Sequence 192, App
39	134.5	8.7	238	3	US-09-461-697-188	Sequence 190, App
40	134.5	8.7	257	3	US-09-461-697-188	Sequence 188, App
41	134.5	8.7	272	3	US-09-461-697-186	Sequence 186, App
42	133.5	8.6	1312	4	US-09-345-882-29	Sequence 573, App
43	133	8.6	567	4	US-09-205-258-573	Sequence 6, Appli
44	132.5	8.5	558	1	US-08-285-440-6	Sequence 6, Appli
45	132.5	8.5	558	1	US-08-630-343-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1  
US-09-828-000-2  
; Sequence 2, Application US/09828000  
; Patent No. 6596690  
; GENERAL INFORMATION:  
; APPLICANT: Government of the United States of America  
; TITLE OF INVENTION: Vasostatin as Marrow Protectant  
; FILE REFERENCE: 4239-55414  
; CURRENT APPLICATION NUMBER: US/09/828,000  
; CURRENT FILING DATE: 2001-04-06  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 416  
; TYPE: PRT  
; ORGANISM: Calreticulin  
US-09-828-000-2

Query Match 99.7%; Score 1549; DB 4; Length 416;  
Best Local Similarity 100.0%; Pred. No. 4.4e-130;  
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GPGTKKHVIFNYKGNVLIN	KDIRCKDD	EFTHTLYTLIVR	PDNTYEVKIDNSQVESGSLE	60
Db	138	GPGTKKHVIFNYKGNVLIN	KDIRCKDD	EFTHTLYTLIVR	PDNTYEVKIDNSQVESGSLE	197
Qy	61	DDWDELPPKKIKPDASK	PDWDERAKID	DOTSKPEDWDKPEHI	PDPAKPEDWDEEM	120
Db	198	DDWDELPPKKIKPDASK	PDWDERAKID	DOTSKPEDWDKPEHI	PDPAKPEDWDEEM	257
Qy	121	DGEWEPPIQNPEYKGEWK	PRQIDNPYKGTWTHPEID	NPESPDPSIYAYDNFVGLD	180	
Db	258	DGEWEPPIQNPEYKGEWK	PRQIDNPYKGTWTHPEID	NPESPDPSIYAYDNFVGLD	317	
Qy	181	LQWQSGTTFDNFLITNDE	AYAEFGNETGWTKAAEKQ	MDKQDEEQR	LKEEBEDKRRK	240
Db	318	LQWQSGTTFDNFLITNDE	AYAEFGNETGWTKAAEKQ	MDKQDEEQR	LKEEBEDKRRK	377
Qy	241	EEEEAEKDEDEKDEE	DEDEDEDEDEDEDE	DEDEDEDEDEDEDE	DEDEDEDEDEDEDE	279
Db	378	EEEEAEKDEDEKDEE	DEDEDEDEDEDEDE	DEDEDEDEDEDEDE	DEDEDEDEDEDEDE	416

RESULT 2  
US-08-675-816-2  
; Sequence 2, Application US/08675816  
; Patent No. 6171864  
; GENERAL INFORMATION:  
; APPLICANT: Coughlan, Sean J.  
; APPLICANT: Winfrey, Jr., Ron J.

;; TITLE OF INVENTION: CALRETICULIN AND CALNEXIN GENES AND PROMOTER REGIONS AND USES

;; NUMBER OF SEQUENCES: 16  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Seed and Berry  
;; STREET: 701 Fifth Ave. Suite 6300  
;; CITY: Seattle  
;; STATE: Washington  
;; COUNTRY: U.S.A.  
;; ZIP: 98104-7092  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/675,816  
;; FILING DATE: 05-JUL-1996  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: No. 6171864tenburg, Carol  
;; REGISTRATION NUMBER: 39,317  
;; REFERENCE/DOCKET NUMBER: 750027.401  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (206)-622-4900  
;; TELEFAX: (206)-682-6031  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 415 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-08-675-816-2

Query Match 55.2%; Score 856.5; DB 3; Length 415;

Best Local Similarity 55.3%; Pred. No. 2.2e-68;

Matches 157; Conservative 36; Mismatches 80; Indels 11; Gaps 4;

QY 1 GPGTKVHVIPNYGKGNVLINIKRDKDFTHTLYTLIVPNDTYEVKIDNSQVSGSL 60

DB 139 GYSTKVKHAILNYNDTHLKEVPCETDQTHVYTLVIRPDATYSFLIDNVEKQTGSL 198

QY 61 DDWFLPKKIDPDASKPDWDERAKIDDPDTSKPEDWDK-PHHIPDPDAKPEDWDER 119

DB 199 TDWLLPPLKKIDPEAKKPDWDEKEVDPEDKKPGYDDIPKPIPDPAKPEDWDDE 258

QY 120 MDGEWPEPVTONPYKGEWPRQIDNDYKGTWHPIDNPYSPPDSIYAYDNFVGL 179

DB 259 EDGEWTAPTIANPEYKGPWKPKIKPNYKGNKAPMIDNPDPKDDPEIVVYVNLKYVGI 318

QY 180 DLWQVKSFTIDNPLIINDAYAEFGNETGWVTKAAEKQMKQKQDEQRLKEEEDKKR 239

DB 319 ELWQVKSFTIDNPLIINDPEYAKQIAEETWGNKQDAEKA---AFEEAEKKKEEESKOD 375

QY 240 KEEBEAEDEKDEDEDEDEDEDEKE---EDEDVPGQAKDEL 280

DB 376 PADSDADEDDDDADTSGEDDGSKSDAEDSAEDV---HDEL 415

## RESULT 3

US-08-296-362-2

Sequence 2, Application US/08296362

Patent No. 5691306

GENERAL INFORMATION:

APPLICANT: Berseron, John J.M.

APPLICANT: Thomas, David Y.

APPLICANT: Waga, Ikuo

TITLE OF INVENTION: METHODS OF DETECTION AND TREATMENT OF

TITLE OF INVENTION: PROTEIN TRAFFICKING DISORDERS AND INCREASING SECRETORY

TITLE OF INVENTION: PROTEIN PRODUCTION

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED AND BERRY

STREET: 6300 Columbia Center, 701 Fifth Avenue

;; CITY: Seattle  
;; STATE: Washington  
;; COUNTRY: US  
;; ZIP: 98104-7092  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/296,362  
;; FILING DATE: 25-AUG-1994  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Deehr, Yanya S.  
;; REGISTRATION NUMBER: 37,120  
;; REFERENCE/DOCKET NUMBER: 690066.401C1  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (206) 622-4900  
;; TELEFAX: (206) 682-6031  
;; TELEX: 3723836  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 593 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-08-296-362-2

Query Match 40.2%; Score 624; DB 1; Length 593;

Best Local Similarity 33.7%; Pred. No. 1.8e-47;

Matches 129; Conservative 58; Mismatches 86; Indels 110; Gaps 8;

QY 6 KVHVFNYKGNVLINKDIRCK-----DDEFTHTLYTLIVPNDTYEVKIDNSOVE 55

DB 200 KUHFIFRHNPKTGVYEEKHAKRPDADIKTYFTDKKHTLYTLINPDNFSFELVDQSLN 259

QY 56 SCSLEDDWDFLP-----KKIKDPDASKPEDWDERAKIDDPDTSKPEDW----- 99

DB 260 SGNLLN--DMTPVPNPSREIEDPEDQKPEDWDERPKIPDPDAVKPDWNEAPAKIPDEE 317

QY 100 -----DKPEHPPDPAKPEDWDEMGKEP-----PVIQON 131

DB 318 ATKPGWLDDDEPVYVPPDAEKPEDWDEMDGWEAPOIANPKCESAPGCGVWQRPMDN 377

QY 132 PSYKGEWPRQIDNDYKGTWHPIDNPYSPPDSIYAYDNFVGLGLDQVKSFTID 191

DB 378 PNYKGNKPPMIDNPYQGIWKPKIPNPDFFEDLEPFKMTFFSAIGLELWSMTSDIFFD 437

QY 192 NPLIINDAYAEFGNETGWVTKAAE-----KQMKDKQDE----- 226

DB 438 NFIVCGRRVVDWANDGWLKKAADGAAPGVVGQMIETAAEERPWLWVYVLTVALPVF 497

QY 227 -----EQLKEEEDK-----KRKEEBAEDKEDDEDDED 257

DB 498 LVISFCCSGKKQSPVEYKKTDAQPQVKEEKEEKEKOKGDEEESGEKLEBKQKSDA 557

QY 258 EDEDEKDEEEDVPGQAKDEL 280

DB 558 BEDGGTASQEDDRKPAEEDDEI 580

## RESULT 4

US-09-976-594-947

Sequence 947, Application US/09976594

Patent No. 6673549

GENERAL INFORMATION:

APPLICANT: Furness, Michael

APPLICANT: Buchbinder, Jenny

TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS

FILE REFERENCE: PA-0041 US

CURRENT APPLICATION NUMBER: US/09/976,594

CURRENT FILING DATE: 2001-10-12

REGISTRATION NUMBER: 39,317  
REFERENCE/DOCKET NUMBER: 750027.401  
TELEPHONE: (206)-622-4900  
TELEFAX: (206)-682-6031  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 542 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-675-816-6

Query Match 31.7%; Score 493; DB 3; Length 542;  
Best Local Similarity 29.8%; Pred. No. 7.6e-36;  
Matches 117; Conservative 41; Mismatches 113; Indels 122; Gaps 10;

QY 1 GP-----GKVKVHVFNYKG--KNVLINKDIR-----CKDDEFTHLTYLIVRPDNTYEVKID 50  
DB 143 GPDKCGATNKVHFKHKNPKSGEVIHHLKYPPSPDKLTHVYTAILKPDNEURLVD 202

QY 51 NSQVESGSLEDDWDLPP---KKIKDPDASKPEDWDERAKIDDPDTSKPEDW----- 99  
DB 203 GEKKKANFLSSDDPEPLVPKATIPDDKKPEDWDERAKIPDPNAVKPDDEADAPME 262

QY 100 -----DKPEHIPDPDAKKPEDWDEMDGEWEPVVIQNP----- 133  
DB 263 IVDEDAEKPEGWLDDEPEBIDDDAAKPEDWDEEDGEWEAPKIDNPKCETAPGCGEWR 322

QY 134 -----YGEWKPRIDNPDYKGTWHPHIDNPY-----SPDPSIYAYDNFVGLGLDLW 182  
DB 323 PMKRNPAKYGKHPALIDNPNYKGIWKPOEIPNPNTFELEKPD-----PEPIAAVGIEIW 377

QY 183 QVKSGETIFDNFLITNDEAYAEFGNETGWTKAAEKQMKDKQD----- 225  
DB 378 TMDGGLIFGHILLADDEKVAESLRQTAKPKFPAEKEKQAEADAAAGSDLAGFKKQVFD 437

QY 226 -----BEQRKKEEEDK----- 243  
DB 438 LLYQVADIPFLSEHKIIDIIEKGEKQPNLTIGILVIVVFTVLFKILFGGKKPAKV 497

RESULT 6  
US-09-828-000-8  
Sequence 8, Application US/09828000  
Patent No. 6596690  
GENERAL INFORMATION:  
APPLICANT: Government of the United States of America  
TITLE OF INVENTION: Vasostatin as Marrow Protectant  
FILE REFERENCE: 4239-55414  
CURRENT APPLICATION NUMBER: US/09/828,000  
CURRENT FILING DATE: 2001-04-06  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: Patent in version 3.0  
SEQ ID NO 8  
LENGTH: 61  
TYPE: PRT  
ORGANISM: Fragment 5  
US-09-828-000-8

Query Match 20.5%; Score 318; DB 4; Length 61;  
Best Local Similarity 100.0%; Pred. No. 1.7e-21;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPCTKKVHVFNYKGVNKLKIDCKDDEFTHLTYLIVRPDNTYEVKIDNSQVESGSL 60  
DB 2 GPCTKKVHVFNYKGVNKLKIDCKDDEFTHLTYLIVRPDNTYEVKIDNSQVESGSL 61

PRIOR APPLICATION NUMBER: 60/240,409  
PRIOR FILING DATE: 2000-10-12  
NUMBER OF SEQ ID NOS: 1143  
SOFTWARE: PERL Program  
SEQ ID NO 947  
LENGTH: 610  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: Incyte ID No. 6673549 3876162CDI  
US-09-976-594-947

Query Match 37.2%; Score 577.5; DB 4; Length 610;  
Best Local Similarity 33.3%; Pred. No. 2.6e-43;  
Matches 127; Conservative 60; Mismatches 83; Indels 111; Gaps 10;

QY 6 KVVHVFNYKGVNKLKIDCK-----DDEFTHLTYLIVRPDNTYEVKIDNSQVE 55  
DB 190 KLFIFRKHHPKTVGFEEKHAKPPDVLKFFTRKTHLYLVNPPDTEVLVDQIVN 249

QY 56 SGSLEDDW--DFLPPKIKDPDASKPEDWDERAKIDDPDTSKPEDW----- 99  
DB 250 KGSLEDDWVVPKPKETIEDNDKKPEWDERAKIPDPSAVKPEDWDESEPAQIEDSSV 309

QY 100 -----DKPEHIPDPDAKKPEDWDEMDGEW-----PPVIONPEYK 135  
DB 310 KPAGWLDDEPFIPDPAEKEDDNNEDTDGEWEAPQILNPACRIGCGEWEKPPMIDNPYK 369

QY 136 GEWKPRIDNPDYKGTWHPHIDNPYSPDSIYAYDNFVGLGLDLWQVSGTIFDNFLI 195  
DB 370 GWRPPLVDNPNYQIWSPRKIPNPDYFEDDHPFLITSFSLGLELNSMTSDIYFDFII 429

QY 196 TNDAYAEFGNETW-----GVTK-----AAB----- 217  
DB 430 CSEKEVACHAAGDGRWKIMIANANKPGVLKQLMAAEGHPWLWLVITAGVPALITS 489

QY 218 -----KQMKDQDEQR-----LKEEEDKKKEE-----EAEKEDDED--K 254  
DB 490 FCWPRKVKKKKDTYKTKDTCIPOTKGVLFQEEKEEKAALKEKPMLEEEKQNDGEMLE 549

QY 255 DEDEDEDEKDEEDVFGQ 275  
DB 550 KEESEPEKSEETETIEGQ 570

RESULT 5  
US-08-675-816-6  
Sequence 6, Application US/08675816  
Patent No. 6171864  
GENERAL INFORMATION:  
APPLICANT: Coughlan, Sean J.  
APPLICANT: Winfrey, Jr., Ron J.  
TITLE OF INVENTION: CALRETICULIN AND CALNEXIN GENES AND PROMOTER REGIONS AND USES  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry  
STREET: 701 Fifth Ave. Suite 6300  
CITY: Seattle  
STATE: Washington  
COUNTRY: U.S.A.  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/675,816  
FILING DATE: 05-JUL-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6171864tenburg, Carol



Qy	242	-----EEAEDKEDDEDKDDEEDKDEEDD-----VP 273
Dd	219	TPAGKKAPAKVVPVKAKNVAEEDDDDEEDDEEDDEEEEEEEEPVKPAP 278
Qy	274	GOAKDEL 280
Dd	279	GKKKKEM 285

RESULT 11  
 US-09-241-333-3  
 ; Sequence 3, Application US/09241333  
 ; Patent No. 6313266  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bandman, Olga  
 ; APPLICANT: Yuse, Henry  
 ; APPLICANT: Corley, Neil C.  
 ; APPLICANT: Shah, Purvi  
 ; TITLE OF INVENTION: HUMAN NUCLEOLIN-LIKE PROTEIN  
 ; NUMBER OF SEQUENCES: 3  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 ; STREET: 3174 Porter Drive  
 ; CITY: Palo Alto  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 94304  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSeq for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/241,333  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/990,114  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Billings, Lucy J.  
 ; REGISTRATION NUMBER: 36,749  
 ; REFERENCE/DOCKET NUMBER: PF-0451 US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 650-855-0555  
 ; TELEFAX: 650-845-4166  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 3:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 714 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; IMMEDIATE SOURCE:  
 ; LIBRARY: GenBank  
 ; CLONE: 128842  
 ; US-09-241-333-3

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Query Match      11.9%; Score 184.5; DB 4; Length 714;
Best Local Similarity 23.9%; Pred. No. 3.4e-08;
Matches 59; Conservative 26; Mismatches 39; Indels 123; Gaps 7;

Qy 67 PPKIKQDASKPEDWDERAKIDPTQSKEDWKEHIFDPDAKPEDWDEMGWEP 126
      ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 129 PAKGAKGNKAKKEDSDSDDDDDSDSDSD-----EEDSEED-EEEP 171
      ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 127 PVIQNPEYKGEWKPRQIDNPDYKGTWHPIDNPYSPOPSIYVDFGLDLQWQKS 186
      ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 172 PVV-----KG-----KQ 178

Qy 187 GTIFNFIITNDAYAEFGNETGVTKYAAKQKMKQDEQRKKEEEDKKRKE----- 241
      ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 179 GKVA-----AAAPASDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEMEI 218
      ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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[illegible]

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RESULT 12
US-08-257-073-5
; Sequence 5, Application US/08257073
; Patent No. 5766597
; GENERAL INFORMATION:
; APPLICANT: Paoletti, Enzo
; APPLICANT: de Taisne, Charles
; APPLICANT: Tine, John A.
; TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE
; NUMBER OF SEQUENCES: 143
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford, P.C.
; STREET: 530 Fifth Avenue, 25th Floor
; CITY: New York
; STATE: New York
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 10036
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/257,073
; FILING DATE: 09-JUN-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/075,783
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/852,305
; FILING DATE: 18-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/672,183
; FILING DATE: 20-MAR-1991
; NAME: Fommer, William S.
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2570
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; TELEX: 425066 CURTMS
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 740 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-08-257-073-5

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Query Match      11.9%; Score 184.5; DB 1; Length 740;
Best Local Similarity 25.3%; Pred. No. 3.5e-08;
Matches 75; Conservative 51; Mismatches 78; Indels 93; Gaps 14

QY      48 KIDNQVBSGLE-----DDWFLPPKKIKD----- 73
Db      457 KEDNQAVTKSWEEPKVQAFALNGVEPTDSNMNSINNVDEIDFFKEKLIENNTFN 516
QY      74 ---PDASXPEDWDZRAK-IDDPDTSKPEDWKEPHFDPAKKXPEDWDZEMDGE----- 123

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Db	246	VGS--SSDGDTPPQPTSPISICSSSPSGSGWGDOTAMLVLAETASAKNKECSN	303
Qy	198	DEAYAEFCNETHVTKAAEQMKQKQDEQRUKKEEEDKKRKEEAEADKEDDEDKQD	257
Db	304	NQA-CEDNGDNIEISKESQVDKQDNKQDEEGETDEDEDEDEDEDEDEDEDEDE	362
Qy	258	EDEDEKDEEED	271
Db	363	EDDEDEDEDEED	376

RESULT 14  
US-09-298-568-2  
; Sequence 2, Application US/09298568

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; Sequence 2, Application US/09298568
; Patent No. 6322792
; GENERAL INFORMATION:
; APPLICANT: Kieff, Elliott D.
; APPLICANT: Balliestas, Mary E.
; APPLICANT: Kaye, Kenneth M.
; TITLE OF INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO
; FILE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE
; FILE REFERENCE: 16412-10001R
; CURRENT APPLICATION NUMBER: US/09/298,568
; CURRENT FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,422
; EARLIER FILING DATE: 1998-11-19
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 2
; LENGTH: 1162
; TYPE: PRT
; ORGANISM: Kaposi's sarcoma-associated herpesvirus
; US-09-298-568-2

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RESULT 15
US-09-410-399-2
; Sequence 2, Application US/09410399
; Patent No. 6482587
; GENERAL INFORMATION:
; APPLICANT: Robertson, Erle S.
; APPLICANT: Cotter, Murray A.
; TITLE OF INVENTION: Methods to Inhibit or Enhance the Binding of Viral DNA
; TITLE OF INVENTION: to genomic Host DNA
; FILE REFERENCE: UM-03778
; CURRENT APPLICATION NUMBER: US/09/410.399
; CURRENT FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 6

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Search completed: October 12, 2004, 15:49:26  
Job time : 21 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 12, 2004, 15:48:36 ; Search time 48 Seconds  
(without alignments)  
1877.162 Million cell updates/sec

Title: US-09-807-148-9

Perfect score: 1553

Sequence: 1 GPGTKVHVIFNKGKVL.....EEDKEDEEDVPGAKDEL 280

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pcp.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pcp.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pcp.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pcp.\*
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- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pcp.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pcp.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pcp.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pcp.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pcp.\*
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- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pcp.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pcp.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pcp.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pcp.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pcp.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1553	100.0	417	10	US-09-906-393A-36
2	1553	100.0	417	14	Sequence 36, Appl
3	1553	100.0	417	15	Sequence 29, Appl
4	1549	99.7	416	10	Sequence 14, Appl
5	1549	99.7	416	15	Sequence 2, Appl
6	1476.5	95.1	416	14	Sequence 2, Appl
7	1476.5	95.1	416	14	Sequence 2, Appl
8	1476.5	95.1	416	14	Sequence 6, Appl
9	991.5	63.8	395	15	Sequence 6343, Ap
10	847	54.5	421	16	Sequence 46544, A
11	844.5	54.4	442	12	Sequence 46869, A
12	844	54.3	346	12	Sequence 48930, A
13	844	54.3	435	12	Sequence 70304, A
14	837.5	53.9	420	9	Sequence 2, Appl
15	835	53.8	431	16	Sequence 44015, A

16	827	53.3	424	16	US-10-437-963-201420	Sequence 201420, A
17	820.5	52.8	268	12	US-10-425-114-38848	Sequence 38848, A
18	810.5	52.2	391	12	US-10-424-599-190956	Sequence 190956, A
19	810.5	52.2	420	12	US-10-424-599-190958	Sequence 190958, A
20	804.5	51.8	391	12	US-10-425-114-46228	Sequence 46228, A
21	804.5	51.8	391	12	US-10-425-114-46228	Sequence 46228, A
22	799.5	51.5	442	16	US-10-437-963-114914	Sequence 114914, A
23	779	50.2	424	16	US-10-437-963-201427	Sequence 201427, A
24	755.5	48.6	388	12	US-10-425-114-46405	Sequence 46405, A
25	755.5	48.6	391	12	US-10-425-114-46405	Sequence 46405, A
26	716.5	46.1	567	16	US-10-437-963-114860	Sequence 114860, A
27	715.5	46.1	422	12	US-10-424-599-277445	Sequence 277445, A
28	715.5	46.1	425	16	US-10-437-963-122222	Sequence 122222, A
29	711.5	45.8	422	16	US-10-767-701-45264	Sequence 45264, A
30	706.5	45.5	418	12	US-10-424-599-153808	Sequence 153808, A
31	704	45.3	434	12	US-10-425-114-70140	Sequence 70140, A
32	703	45.3	439	12	US-10-425-114-75495	Sequence 75495, A
33	702.5	45.2	434	12	US-10-425-114-75498	Sequence 75498, A
34	649.5	41.8	372	12	US-10-425-114-44621	Sequence 44621, A
35	649.5	41.8	372	12	US-10-425-114-44997	Sequence 44997, A
36	629	40.5	591	14	US-10-205-194-129	Sequence 129, App
37	628	40.4	592	16	US-10-408-765A-1095	Sequence 1095, Ap
38	617	39.7	207	12	US-10-425-114-56908	Sequence 56908, A
39	577.5	37.2	610	14	US-10-205-823-68	Sequence 68, Appl
40	555.5	35.8	184	16	US-10-767-701-61049	Sequence 61049, A
41	549.5	35.4	390	15	US-10-161-927-46	Sequence 46, Appl
42	518.5	33.4	167	16	US-10-767-701-55857	Sequence 55857, A
43	506.5	32.6	536	12	US-10-425-114-40444	Sequence 40444, A
44	501.5	32.3	536	16	US-10-767-701-47162	Sequence 47162, A
45	492.5	31.7	537	16	US-10-437-963-146333	Sequence 146333, A

ALIGNMENTS

RESULT 1  
US-09-906-393A-36  
; Sequence 36, Application US/09906393A  
; Publication No. US20030039970A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Zhou  
; APPLICANT: Xiao, Wuhan  
; TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED  
; FILE REFERENCE: 1720-1-001CIP  
; CURRENT APPLICATION NUMBER: US/09/906,393A  
; CURRENT FILING DATE: 2001-07-16  
; PRIOR APPLICATION NUMBER: 60/218,761  
; PRIOR FILING DATE: 2000-07-17  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 36  
; TYPE: PRT  
; LENGTH: 417  
; ORGANISM: Homo sapiens  
US-09-906-393A-36

Query Match	100.0%;	Score 1553;	DB 10;	Length 417;
Best Local Similarity	100.0%;	Pred. No. 1e-106;		
Matches 280;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
Qy	1	GPCTKVVHVFYFNKGKVLINCKDDEFFHLYTLIVRPDNTYEVKIDNSQVSGSLE	60	
Db	138	GPCTKVVHVFYFNKGKVLINCKDDEFFHLYTLIVRPDNTYEVKIDNSQVSGSLE	197	
Qy	61	DDWDFLPPKKIKDPDASKPEDWDERAKIDDPDTSKPEDWKPDPDPAKPEDWDEEM	120	
Db	198	DDWDFLPPKKIKDPDASKPEDWDERAKIDDPDTSKPEDWKPDPDPAKPEDWDEEM	257	
Qy	121	DGWESEPVTONPEYKGEWKPRQIDNPDYKGTWTHPBDNPEYSPDPSIYAYDNFVGLGD	180	
Db	258	DGWESEPVTONPEYKGEWKPRQIDNPDYKGTWTHPBDNPEYSPDPSIYAYDNFVGLGD	317	
Qy	181	LWQVSGTTPFNDPLIINDAEYAEFGNETGWVTGVTAAAEKQMKQDQEORLKSEEDKKRK	240	

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; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-093-14

Query Match      100.0%; Score 1553; DB 14; Length 417;
Best Local Similarity 100.0%; Pred. No. 1e-106;
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGTKKHVIFNYKGNVLINKDIRCKDDDETHLYTLIVRPDNTYEVKIDNSQVESGSL 60
DB 138 GPGTKKHVIFNYKGNVLINKDIRCKDDDETHLYTLIVRPDNTYEVKIDNSQVESGSL 197
QY 61 DDWDFLPPKKIKDPDASKPEDWDERAKIDDDPTDSKPEDWDPKPEHIPDPDAKKPEDWDEEM 120
DB 198 DDWDFLPPKKIKDPDASKPEDWDERAKIDDDPTDSKPEDWDPKPEHIPDPDAKKPEDWDEEM 257
QY 121 DGEWEPPIQNPYKGEWKPRQIDNPDKGTWHPIDNPYSDPSIAYDNFGVLGLD 180
DB 258 DGEWEPPIQNPYKGEWKPRQIDNPDKGTWHPIDNPYSDPSIAYDNFGVLGLD 317
QY 181 LQVKSGETIFDNFLITNDEAYAEFGNETGWVTKAAEKQMKDKQDEBQRLKEEEDKKRK 240
DB 318 LQVKSGETIFDNFLITNDEAYAEFGNETGWVTKAAEKQMKDKQDEBQRLKEEEDKKRK 377

RESULT 2
US-10-161-959-29
; Sequence 29, Application US/10161959
; Publication No. US20030096748A1
; GENERAL INFORMATION:
; APPLICANT: Holoshitz, Joseph
; APPLICANT: Ling, Song
; TITLE OF INVENTION: Methods and Compositions for the Treatment of Diseases Associated
; FILE REFERENCE: UM-07135
; CURRENT APPLICATION NUMBER: US/10/161,959
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 60/295,691
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 29
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-161-959-29

Query Match      100.0%; Score 1553; DB 14; Length 417;
Best Local Similarity 100.0%; Pred. No. 1e-106;
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGTKKHVIFNYKGNVLINKDIRCKDDDETHLYTLIVRPDNTYEVKIDNSQVESGSL 60
DB 138 GPGTKKHVIFNYKGNVLINKDIRCKDDDETHLYTLIVRPDNTYEVKIDNSQVESGSL 197
QY 61 DDWDFLPPKKIKDPDASKPEDWDERAKIDDDPTDSKPEDWDPKPEHIPDPDAKKPEDWDEEM 120
DB 198 DDWDFLPPKKIKDPDASKPEDWDERAKIDDDPTDSKPEDWDPKPEHIPDPDAKKPEDWDEEM 257
QY 121 DGEWEPPIQNPYKGEWKPRQIDNPDKGTWHPIDNPYSDPSIAYDNFGVLGLD 180
DB 258 DGEWEPPIQNPYKGEWKPRQIDNPDKGTWHPIDNPYSDPSIAYDNFGVLGLD 317
QY 181 LQVKSGETIFDNFLITNDEAYAEFGNETGWVTKAAEKQMKDKQDEBQRLKEEEDKKRK 240
DB 318 LQVKSGETIFDNFLITNDEAYAEFGNETGWVTKAAEKQMKDKQDEBQRLKEEEDKKRK 377

RESULT 3
US-10-367-093-14
; Sequence 14, Application US/10367093
; Publication No. US20030216315A1
; GENERAL INFORMATION:
; APPLICANT: Duke University
; APPLICANT: Nicchitta, Chris
; APPLICANT: Baker-LePain, Julie
; TITLE OF INVENTION: MODULATION OF IMMUNE RESPONSE BY NON-PEPTIDE BINDING STRESS RESPO
; FILE REFERENCE: 180/145
; CURRENT APPLICATION NUMBER: US/10/367,093
; CURRENT FILING DATE: 2003-02-13
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 14
```

```

; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-093-14

Query Match      100.0%; Score 1553; DB 15; Length 417;
Best Local Similarity 100.0%; Pred. No. 1e-106;
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGTKKHVIFNYKGNVLINKDIRCKDDDETHLYTLIVRPDNTYEVKIDNSQVESGSL 60
DB 138 GPGTKKHVIFNYKGNVLINKDIRCKDDDETHLYTLIVRPDNTYEVKIDNSQVESGSL 197
QY 61 DDWDFLPPKKIKDPDASKPEDWDERAKIDDDPTDSKPEDWDPKPEHIPDPDAKKPEDWDEEM 120
DB 198 DDWDFLPPKKIKDPDASKPEDWDERAKIDDDPTDSKPEDWDPKPEHIPDPDAKKPEDWDEEM 257
QY 121 DGEWEPPIQNPYKGEWKPRQIDNPDKGTWHPIDNPYSDPSIAYDNFGVLGLD 180
DB 258 DGEWEPPIQNPYKGEWKPRQIDNPDKGTWHPIDNPYSDPSIAYDNFGVLGLD 317
QY 181 LQVKSGETIFDNFLITNDEAYAEFGNETGWVTKAAEKQMKDKQDEBQRLKEEEDKKRK 240
DB 318 LQVKSGETIFDNFLITNDEAYAEFGNETGWVTKAAEKQMKDKQDEBQRLKEEEDKKRK 377

RESULT 4
US-09-828-000-2
; Sequence 2, Application US/09828000
; Publication No. US20030078198A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 2
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Calreticulin
US-09-828-000-2

Query Match      99.7%; Score 1549; DB 10; Length 416;
Best Local Similarity 100.0%; Pred. No. 2e-106;
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGTKKHVIFNYKGNVLINKDIRCKDDDETHLYTLIVRPDNTYEVKIDNSQVESGSL 60
DB 138 GPGTKKHVIFNYKGNVLINKDIRCKDDDETHLYTLIVRPDNTYEVKIDNSQVESGSL 197
QY 61 DDWDFLPPKKIKDPDASKPEDWDERAKIDDDPTDSKPEDWDPKPEHIPDPDAKKPEDWDEEM 120
DB 198 DDWDFLPPKKIKDPDASKPEDWDERAKIDDDPTDSKPEDWDPKPEHIPDPDAKKPEDWDEEM 257
QY 121 DGEWEPPIQNPYKGEWKPRQIDNPDKGTWHPIDNPYSDPSIAYDNFGVLGLD 180
DB 258 DGEWEPPIQNPYKGEWKPRQIDNPDKGTWHPIDNPYSDPSIAYDNFGVLGLD 317
QY 181 LQVKSGETIFDNFLITNDEAYAEFGNETGWVTKAAEKQMKDKQDEBQRLKEEEDKKRK 240
DB 318 LQVKSGETIFDNFLITNDEAYAEFGNETGWVTKAAEKQMKDKQDEBQRLKEEEDKKRK 377

241 EEEAEADKEDDEDKDEDEEDKEEEDKEEEDVPGQAKDE 280
378 EEEAEADKEDDEDKDEDEEDKEEEDKEEEDVPGQAKDE 417
```

RESULT 5  
US-10-405-588-2  
; Sequence 2, Application US/10405588  
; Publication No. US20030216299A1  
; GENERAL INFORMATION:  
; APPLICANT: Government of the United States of America  
; TITLE OF INVENTION: Vasostatin as Marrow Protectant  
; FILE REFERENCE: 4239-55414  
; CURRENT APPLICATION NUMBER: US/10/405.588  
; CURRENT FILING DATE: 2003-04-01  
; PRIOR APPLICATION NUMBER: US/09/828,000  
; PRIOR FILING DATE: 2001-04-06  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 2  
; LENGTH: 416  
; TYPE: PRT  
; ORGANISM: Calreticulin  
US-10-405-588-2

Query Match 99.7%; Score 1549; DB 15; Length 416;  
Best Local Similarity 100.0%; Pred. No. 2e-106;  
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPGTKKVHVI FNYKGNVLINKDIRCKDDEFTHLTVLRPDNTYEVKIDNSQVESGSL 60  
Db 138 GPGTKKVHVI FNYKGNVLINKDIRCKDDEFTHLTVLRPDNTYEVKIDNSQVESGSL 197

Qy 61 DDWDFLPPKKIKDPDASKPEDWDERAKIDDDPTDSKPEDWDPKEHIPDPDAKPPEDWDEEM 120  
Db 198 DDWDFLPPKKIKDPDASKPEDWDERAKIDDDPTDSKPEDWDPKEHIPDPDAKPPEDWDEEM 257

Qy 121 DGEWEPPIQNPPEYKGEWKPRQIDNPDKYKGTWHPIDNPPEYSPDPSIYAYDNFVGLGD 180  
Db 258 DGEWEPPIQNPPEYKGEWKPRQIDNPDKYKGTWHPIDNPPEYSPDPSIYAYDNFVGLGD 317

Qy 181 LWQVKSGTIFDNFLITNDEAYAEFGNETGWTKAAEKQMKDKQDEQRLEKEEEDKKRK 240  
Db 318 LWQVKSGTIFDNFLITNDEAYAEFGNETGWTKAAEKQMKDKQDEQRLEKEEEDKKRK 377

Qy 241 EEEAEADKEDDE 280  
Db 378 EEEAEADKEDDE 416

RESULT 7  
US-10-316-253-4  
; Sequence 4, Application US/10316253  
; Publication No. US20030162706A1  
; GENERAL INFORMATION:  
; APPLICANT: The Procter & Gamble Company  
; APPLICANT: Peters, Kevin  
; APPLICANT: Thompson, Larry  
; APPLICANT: Wang, Feng  
; APPLICANT: Greis, Kenneth  
; TITLE OF INVENTION: Angiogenesis Modulating Proteins  
; FILE REFERENCE: 8865M  
; CURRENT APPLICATION NUMBER: US/10/316,253  
; CURRENT FILING DATE: 2002-12-10  
; PRIOR APPLICATION NUMBER: US 60/355,295  
; PRIOR FILING DATE: 2002-02-08  
; NUMBER OF SEQ ID NOS: 308  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 4  
; LENGTH: 416  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
US-10-316-253-4

Query Match 95.1%; Score 1476.5; DB 14; Length 416;  
Best Local Similarity 94.6%; Pred. No. 4.6e-101;  
Matches 265; Conservative 10; Mismatches 4; Indels 1; Gaps 1;

Qy 1 GPGTKKVHVI FNYKGNVLINKDIRCKDDEFTHLTVLRPDNTYEVKIDNSQVESGSL 60  
Db 138 GPGTKKVHVI FNYKGNVLINKDIRCKDDEFTHLTVLRPDNTYEVKIDNSQVESGSL 197

Qy 61 DDWDFLPPKKIKDPDASKPEDWDERAKIDDDPTDSKPEDWDPKEHIPDPDAKPPEDWDEEM 120  
Db 198 DDWDFLPPKKIKDPDASKPEDWDERAKIDDDPTDSKPEDWDPKEHIPDPDAKPPEDWDEEM 257

Qy 121 DGEWEPPIQNPPEYKGEWKPRQIDNPDKYKGTWHPIDNPPEYSPDPSIYAYDNFVGLGD 180  
Db 258 DGEWEPPIQNPPEYKGEWKPRQIDNPDKYKGTWHPIDNPPEYSPDPSIYAYDNFVGLGD 317

Qy 181 LWQVKSGTIFDNFLITNDEAYAEFGNETGWTKAAEKQMKDKQDEQRLEKEEEDKKRK 240  
Db 318 LWQVKSGTIFDNFLITNDEAYAEFGNETGWTKAAEKQMKDKQDEQRLEKEEEDKKRK 377

Qy 241 EEEAEADKEDDE 280  
Db 378 EEEAEADKEDDE 416

RESULT 8  
US-10-316-253-6  
; Sequence 6, Application US/10316253

RESULT 6  
US-10-316-253-2  
; Sequence 2, Application US/10316253  
; Publication No. US20030162706A1  
; GENERAL INFORMATION:  
; APPLICANT: The Procter & Gamble Company  
; APPLICANT: Peters, Kevin  
; APPLICANT: Thompson, Larry  
; APPLICANT: Wang, Feng  
; APPLICANT: Greis, Kenneth  
; TITLE OF INVENTION: Angiogenesis Modulating Proteins  
; FILE REFERENCE: 8865M  
; CURRENT APPLICATION NUMBER: US/10/316,253  
; CURRENT FILING DATE: 2002-12-10  
; PRIOR APPLICATION NUMBER: US 60/355,295  
; PRIOR FILING DATE: 2002-02-08  
; NUMBER OF SEQ ID NOS: 308  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 2  
; LENGTH: 416  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
US-10-316-253-2

Query Match 95.1%; Score 1476.5; DB 14; Length 416;  
Best Local Similarity 94.6%; Pred. No. 4.6e-101;  
Matches 265; Conservative 10; Mismatches 4; Indels 1; Gaps 1;

Qy 1 GPGTKKVHVI FNYKGNVLINKDIRCKDDEFTHLTVLRPDNTYEVKIDNSQVESGSL 60  
Db 138 GPGTKKVHVI FNYKGNVLINKDIRCKDDEFTHLTVLRPDNTYEVKIDNSQVESGSL 197

Qy 61 DDWDFLPPKKIKDPDASKPEDWDERAKIDDDPTDSKPEDWDPKEHIPDPDAKPPEDWDEEM 120  
Db 198 DDWDFLPPKKIKDPDASKPEDWDERAKIDDDPTDSKPEDWDPKEHIPDPDAKPPEDWDEEM 257

Qy 121 DGEWEPPIQNPPEYKGEWKPRQIDNPDKYKGTWHPIDNPPEYSPDPSIYAYDNFVGLGD 180  
Db 258 DGEWEPPIQNPPEYKGEWKPRQIDNPDKYKGTWHPIDNPPEYSPDPSIYAYDNFVGLGD 317

Qy 181 LWQVKSGTIFDNFLITNDEAYAEFGNETGWTKAAEKQMKDKQDEQRLEKEEEDKKRK 240  
Db 318 LWQVKSGTIFDNFLITNDEAYAEFGNETGWTKAAEKQMKDKQDEQRLEKEEEDKKRK 377

Qy 241 EEEAEADKEDDE 279  
Db 378 EEEAEADKEDDE 416

Publication No. US20030162706A1  
 GENERAL INFORMATION:  
 APPLICANT: The Procter & Gamble Company  
 APPLICANT: Peters, Kevin  
 APPLICANT: Thompson, Larry  
 APPLICANT: Wang, Feng  
 APPLICANT: Greis, Kenneth  
 TITLE OF INVENTION: Angiogenesis Modulating Proteins  
 FILE REFERENCE: 8865M  
 CURRENT APPLICATION NUMBER: US/10/316,253  
 CURRENT FILING DATE: 2002-12-10  
 PRIOR APPLICATION NUMBER: US 60/355,295  
 PRIOR FILING DATE: 2002-02-08  
 NUMBER OF SEQ ID NOS: 308  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 6  
 LENGTH: 416  
 TYPE: PRT  
 ORGANISM: Rattus norvegicus  
 US-10-316-253-6

Query Match 95.1%; Score 1476.5; DB 14; Length 416;  
 Best Local Similarity 94.6%; Pred. No. 4.6e-101;  
 Matches 265; Conservative 10; Mismatches 4; Indels 1; Gaps 1;

QY 1 GPGTKKHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 60  
 DB 138 GPGTKKHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 197

QY 61 DDWDFLPPKKIKDPDASKPDWDERAKIDDDPTDSKPDWDKPEHIPDPDAKPEDWDEEM 120  
 DB 198 DDWDFLPPKKIKDPAKPEDWDERAKIDDDPTDSKPDWDKPEHIPDPDAKPEDWDEEM 257

QY 121 DGEWPPVQNPYKGEWKPKQIDNPDKGTWTHPEIDNPYSPDPSIYAYDNFVGLGD 180  
 DB 258 DGEWPPVQNPYKGEWKPKQIDNPDKGTWTHPEIDNPYSPDPSIYAYDNFVGLGD 317

QY 181 LMQVKSGLTFIDNLTNDDEAYAEFGNETGWTKAAEKQMKDKODEEORLKEEEDKKR 240  
 DB 318 LMQVKSGLTFIDNLTNDDEAYAEFGNETGWTKAAEKQMKDKODEEORLKEEEDKKR 377

QY 241 EEEAEKDEDEDDE 280  
 DB 378 EEEAEKDEDEDDE 416

RESULT 9  
 US-10-369-493-6343  
 Sequence 6343, Application US/10369493  
 Publication No. US20030233675A1  
 GENERAL INFORMATION:  
 APPLICANT: Cao, Yongwei  
 APPLICANT: Hinkle, Gregory J.  
 APPLICANT: Slater, Steven C.  
 APPLICANT: Goldman, Barry S.  
 APPLICANT: Chen, Xianfeng  
 TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
 TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES  
 FILE REFERENCE: 38-10(52052)B  
 CURRENT APPLICATION NUMBER: US/10/369,493  
 CURRENT FILING DATE: 2003-02-28  
 PRIOR APPLICATION NUMBER: US 60/360,039  
 PRIOR FILING DATE: 2002-02-21  
 NUMBER OF SEQ ID NOS: 47374  
 SEQ ID NO 6343  
 LENGTH: 395  
 TYPE: PRT  
 ORGANISM: Caenorhabditis elegans  
 US-10-369-493-6343

Query Match 63.8%; Score 991.5; DB 15; Length 395;  
 Best Local Similarity 66.0%; Pred. No. 2.8e-65;  
 Matches 173; Conservative 35; Mismatches 53; Indels 1; Gaps 1;

QY 1 GPGTKKHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 60  
 DB 134 GP-TRRVHVLINYNKGENKLIKKEITCKSDELTHLYTLILNSDNTYEVKIDGESAGTGSLE 192

QY 61 DDWDFLPPKKIKDPDASKPDWDERAKIDDDPTDSKPDWDKPEHIPDPDAKPEDWDEEM 120  
 DB 193 EDWDLPLPAKKIKDPDAKPEDWDEREYIDDAEDAKPEDWKEPHEIPDPDAKPEDWDEEM 252

QY 121 DGEWPPVQNPYKGEWKPKQIDNPDKGTWTHPEIDNPYSPDPSIYAYDNFVGLGD 180  
 DB 253 DGEWPPVQNPYKGEWKPKQIDNPDKGTWTHPEIDNPYSPDPSIYAYDNFVGLGD 312

QY 181 LMQVKSGLTFIDNLTNDDEAYAEFGNETGWTKAAEKQMKDKODEEORLKEEEDKKR 240  
 DB 313 LMQVKSGLTFIDNLTNDDEAYAEFGNETGWTKAAEKQMKDKODEEORLKEEEDKKR 372

QY 241 EEEAEKDEDEDDE 262  
 DB 373 EEEAEKDEDEDDE 394

RESULT 10  
 US-10-767-701-46544  
 Sequence 46544, Application US/10767701  
 Publication No. US20040172884A1  
 GENERAL INFORMATION:  
 APPLICANT: Kovalic, David K.  
 APPLICANT: Zhou, Yihua  
 APPLICANT: Cao, Yongwei  
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
 TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement  
 FILE REFERENCE: 38-21(53535)B  
 CURRENT APPLICATION NUMBER: US/10/767,701  
 CURRENT FILING DATE: 2004-01-29  
 NUMBER OF SEQ ID NOS: 63128  
 SEQ ID NO 46544  
 LENGTH: 421  
 TYPE: PRT  
 ORGANISM: Sorghum bicolor  
 FEATURE:  
 OTHER INFORMATION: Clone ID: SORBI-28MAY03-CS075\_1.pep  
 US-10-767-701-46544

Query Match 54.5%; Score 847; DB 16; Length 421;  
 Best Local Similarity 54.4%; Pred. No. 1.4e-54;  
 Matches 154; Conservative 45; Mismatches 76; Indels 8; Gaps 4;

QY 1 GPGTKKHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 60  
 DB 144 GYSTKRVHTILTKDGNHLIKKQVPCETDQLTHVTVTLIRPDATYSLIDNEEKQTGSY 203

QY 61 DDWDFLPPKKIKDPDASKPDWDERAKIDDDPTDSKPDWDKPEHIPDPDAKPEDWDEEM 119  
 DB 204 EHWDLPLPAKKIKDPDAKPEDWDEREYIDDAEDAKPEDWKEPHEIPDPDAKPEDWDEEM 263

QY 120 MDGEWPPVQNPYKGEWKPKQIDNPDKGTWTHPEIDNPYSPDPSIYAYDNFVGLGD 179  
 DB 264 EDGEWTATIPNPYKGEWKPKQIDNPDKGTWTHPEIDNPYSPDPSIYAYDNFVGLGD 323

QY 180 DLWQVKSGLTFIDNLTNDDEAYAEFGNETGWTKAAEKQMKDKODEEORLKEEEDKKR 238  
 DB 324 ELWQVKSGLTFIDNLTNDDEAYAEFGNETGWTKAAEKQMKDKODEEORLKEEEDKKR 380

QY 239 -RKEEEAEKDEDEDDE 280  
 DB 381 GDEDDDE 421

RESULT 11  
 US-10-425-114-46869  
 Sequence 46869, Application US/10425114  
 Publication No. US20040034888A1

```

; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 46869
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73073A05_FLI.pep
US-10-425-114-46869

Query Match 54.4%; Score 844.5; DB 12; Length 442;
Best Local Similarity 53.0%; Pred. No. 2.3e-54;
Matches 149; Conservative 49; Mismatches 78; Indels 5; Gaps 2;

QY 1 GPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHLTYTLIVRPDNTYEVKIDNSQVSGSLE 60
DB 166 GYSTKKVHTILTCKGNHLIKKQVPCETDQLTHVYTLIRPDATYSILIDNEKQTSIY 225

QY 61 DWDWFLPPKTKDPPDASKPEDWDERAKIDDDPTDSKPEDWK-PHIHPDPAKPEDWDEE 119
DB 226 EHWDLILPPKTKDPPDASKPEDWDDKEYIPDPEDKKEGYDDIPKEIPDPAKPEDWDE 285

QY 120 MDGEWEPPIQNPYKGEWKPRQIDNPDKYKTGTHPEIDNPESPDPSIAYDNFVGL 179
DB 286 EDGEWTAIPTNPYKGPWKQKKIKPNYQGWKAPMIDNPDYKDDYIYAFDSLKYIGI 345

QY 180 DLQVKSGLTIFDNFLITNDEAYAEFGNETGWVTKAAEQMKDKODEEQLKEEEDKKR 239
DB 346 ELQVKSGLTIFDNFLITNDEAYAEFGNETGWVTKAAEQMKDKODEEQLKEEEDKKR 401

QY 240 KEEEAEDKEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 280
DB 402 GGDEDDDDLEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 442

RESULT 12
US-10-425-114-48930
; Sequence 48930, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 48930
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3150-081-A9_FLI.pep
US-10-425-114-48930

Query Match 54.3%; Score 844; DB 12; Length 346;
Best Local Similarity 53.7%; Pred. No. 1.9e-54;
Matches 154; Conservative 46; Mismatches 71; Indels 16; Gaps 5;

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Matches 154; Conservative 46; Mismatches 71; Indels 16; Gaps 5;

QY 1 GPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHLTYTLIVRPDNTYEVKIDNSQVSGSLE 60
DB 69 GYSTKKVHTILTCKGNHLIKKQVPCETDQLTHVYTLIRPDATYSILIDNEKQTSIY 128

QY 61 DWDWFLPPKTKDPPDASKPEDWDERAKIDDDPTDSKPEDWK-PHIHPDPAKPEDWDEE 119
DB 129 EHWDLILPPKTKDPPDASKPEDWDDKEYIPDPEDKKEGYDDIPKEIPDPAKPEDWDE 188

QY 120 MDGEWEPPIQNPYKGEWKPRQIDNPDKYKTGTHPEIDNPESPDPSIAYDNFVGL 179
DB 189 EDGEWTAIPTNPYKGPWKQKKIKPNYQGWKAPMIDNPDYKDDYIYAFDSLKYIGI 248

QY 180 DLQVKSGLTIFDNFLITNDEAYAEFGNETGWVTKAAEQMKDKODEEQLKEEEDKKR 239
DB 249 ELQVKSGLTIFDNFLITNDEAYAEFGNETGWVTKAAEQMKDKODEEQLKEEEDKKR 304

QY 240 ---KEEEAEDKEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 280
DB 305 GGDEDDDDLEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 346

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RESULT 13
US-10-425-114-70304
; Sequence 70304, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 70304
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Zea mays subsp. mexicana
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMROTEOSINTE102C08_FLI.pep
US-10-425-114-70304

Query Match 54.3%; Score 844; DB 12; Length 435;
Best Local Similarity 53.7%; Pred. No. 2.4e-54;
Matches 154; Conservative 46; Mismatches 71; Indels 16; Gaps 5;

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QY 1 GPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHLTYTLIVRPDNTYEVKIDNSQVSGSLE 60
DB 158 GYSTKKVHTILTCKGNHLIKKQVPCETDQLTHVYTLIRPDATYSILIDNEKQTSIY 217

QY 61 DWDWFLPPKTKDPPDASKPEDWDERAKIDDDPTDSKPEDWK-PHIHPDPAKPEDWDEE 119
DB 218 EHWDLILPPKTKDPPDASKPEDWDDKEYIPDPEDKKEGYDDIPKEIPDPAKPEDWDE 277

QY 120 MDGEWEPPIQNPYKGEWKPRQIDNPDKYKTGTHPEIDNPESPDPSIAYDNFVGL 179
DB 278 EDGEWTAIPTNPYKGPWKQKKIKPNYQGWKAPMIDNPDYKDDYIYAFDSLKYIGI 337

QY 180 DLQVKSGLTIFDNFLITNDEAYAEFGNETGWVTKAAEQMKDKODEEQLKEEEDKKR 239
DB 338 ELQVKSGLTIFDNFLITNDEAYAEFGNETGWVTKAAEQMKDKODEEQLKEEEDKKR 393

QY 240 ---KEEEAEDKEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 280
DB 394 GGDEDDDDLEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 435

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## RESULT 14

US-09-844-006A-2  
 ; Sequence 2, Application US/09844006A  
 ; Patent No. US20020083496A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wyatt, Sarah  
 ; APPLICANT: Tsoi, Pei-Lan  
 ; APPLICANT: Robertson, Dominique  
 ; APPLICANT: Boss, Wendy  
 ; TITLE OF INVENTION: TRANSGENIC PLANTS WITH INCREASES IN CALCIUM STORES  
 ; FILE REFERENCE: 5051.503  
 ; CURRENT APPLICATION NUMBER: US/09/844.006A  
 ; CURRENT FILING DATE: 2001-04-30  
 ; PRIOR APPLICATION NUMBER: 60/200,233  
 ; PRIOR FILING DATE: 2000-04-28  
 ; NUMBER OF SEQ ID NOS: 8  
 ; SOFTWARE: Patent in version 3.0  
 ; SEQ ID NO 2  
 ; LENGTH: 420  
 ; TYPE: PRT  
 ; ORGANISM: Zea mays  
 US-09-844-006A-2

Query Match 53.9%; Score 837.5; DB 9; Length 420;  
 Best Local Similarity 52.9%; Pred. No. 7.1e-54;  
 Matches 147; Conservative 49; Mismatches 77; Indels 5; Gaps 2;

QY 4 TKKVHVIFNYKGNVLINKDIRCKDDSEFTHLYTLIVRPDNTYEVKIDNSQVESGSLEDDW 63  
 DB 147 TKVHTLTDKGNHLIKKQVPCDTDLTHVYTLIRPDATYSLIDNEEKTCGSIYEHW 206  
 QY 64 DFLPPKKIKDPDASKPEDWDERAKIDDPDTSKPEDWDK-PEHIPDPDAKPEDWDEMDG 122  
 DB 207 DILPPKKIKDPEAKPEDWDKKEYIPDPEDKPKPGYDDIPKEIPDPDAKPEDWDEEDG 266  
 QY 123 EWEPPVTONPYKGEWKPRQIDNPDYKGTWHPIDNPEYSPDPSIYAYDNFVGLDLW 182  
 DB 267 EWTAPTIPNPEYKGPWKQKKIKPNYQGWKAPMIDNPDPKDDPYIYAFDSLKYIGIELW 326  
 QY 183 QVKSGLTFDNLIITNDAYAEFGNETGWVTKAAEKQMKDKQDEEQRLEKEEEDKKRKEE 242  
 DB 327 QVKSGLTFDNLIITDDPALAKTFAEETWKGKKEAKAFADEAK- ----KKEEEDAAKGGD 382  
 QY 243 EAEDEKDE 280  
 DB 383 DEDDDLEDE 420

## RESULT 15

US-10-767-701-44015  
 ; Sequence 44015, Application US/10767701  
 ; Publication No. US20040172684A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kovalic, David K.  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Cao, Yongwei  
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
 ; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement  
 ; FILE REFERENCE: 38-21(53535)B  
 ; CURRENT APPLICATION NUMBER: US/10/767,701  
 ; CURRENT FILING DATE: 2004-01-29  
 ; NUMBER OF SEQ ID NOS: 63128  
 ; SEQ ID NO 44015  
 ; LENGTH: 431  
 ; TYPE: PRT  
 ; ORGANISM: Sorghum bicolor  
 ; FEATURE:  
 ; NAME/KEY: unsure  
 ; LOCATION: (1) -- (431)  
 ; OTHER INFORMATION: unsure at all Xaa locations  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C10317\_1.pap  
 US-10-767-701-44015

Query Match 53.8%; Score 835; DB 16; Length 431;  
 Best Local Similarity 54.3%; Pred. No. 1.1e-53;  
 Matches 159; Conservative 35; Mismatches 75; Indels 24; Gaps 5;  
 QY 1 GPGTKKVHVIFNYKGNVLINKDIRCKDDSEFTHLYTLIVRPDNTYEVKIDNSQVESGSLE 60  
 DB 150 GYATKKVHAILTKGNHLLIKELPGETDQLTHVYTLIRPDATYSLIDNDEKQSGSIY 209  
 QY 61 DDWDFLPPKKIKDPDASKPEDWDERAKIDDPDTSKPEDWDK-PEHIPDPDAKPEDWDEE 119  
 DB 210 DDWDFLPPKKIKDPDASKPEDWDDKEYIPDPEDKPKPGYDDIPKEIPDPDAKPEDWDE 269  
 QY 120 MDGEWEPVTONPYKGEWKPRQIDNPDYKGTWHPIDNPEYSPDPSIYAYDNFVGLGL 179  
 DB 270 EDGEWTAPTIPNPEYKGPWKQKKIKPNPYKGNKAPLIDNPDPKDDPYIYAFDSLKHIGI 329  
 QY 180 DLWQVKSGLTFDNLIITNDAYAEFGNETGWVTKAAEKQMKDKQDEEQRLEKEEEDKKR 239  
 DB 330 ELWQVKSGLTFDNLIITDDPEYAKKLAVETWKGKDAEKAADF-----EAEKKR 378  
 QY 240 KEE-----EAEDEKEDDE--DKDEDEDEDE-----KEEEDDEEVPGQAKDEL 280  
 DB 379 LEECFSLXESASSKODDDLDVDEDEDDADDKADHSDTDEADESEAKHDEL 431

Search completed: October 12, 2004, 15:54:17  
 Job time : 50 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 12, 2004, 15:46:05 ; Search time 17 Seconds  
(without alignments)  
1584.331 Million cell updates/sec

Title: US-09-807-148-9  
Perfect score: 1553  
Sequence: 1 GFGTKVHVIFNYKKNVLI.....BEDKEDEEDVPCQAKDEL 280

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191536 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 78:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1553	100.0	417	1 A37047	calreticulin precu
2	1487.5	95.8	416	1 S08763	calreticulin precu
3	1476.5	95.1	416	1 JH0819	calreticulin precu
4	1457.5	93.9	418	1 A34154	calreticulin precu
5	1442	92.9	400	2 S43376	calreticulin, brai
6	1432	92.2	421	2 S35799	calreticulin precu
7	1280.5	82.5	411	2 S29129	calreticulin precu
8	1249.5	80.5	384	2 S29130	calreticulin (clon
9	1241.5	79.9	419	2 S71343	calreticulin precu
10	1184	75.0	405	1 JH0795	calreticulin precu
11	1031.5	66.4	406	2 A56637	calreticulin homol
12	991.5	63.8	395	2 S25951	calreticulin precu
13	944.5	60.8	336	2 A32507	41K larval antigen
14	856.5	55.2	415	2 T10172	calreticulin - cas
15	844	54.3	421	2 S58170	calreticulin precu
16	818.5	52.7	416	2 T15968	calreticulin call
17	817.5	52.6	389	2 T03691	calreticulin - com
18	817.5	52.6	393	1 A48573	calreticulin autoa
19	814.5	52.4	416	2 T14554	calreticulin - bee
20	813	52.4	422	2 T07841	probable calreticu
21	812	52.3	415	2 T05703	calreticulin - bar
22	812	52.3	412	2 T05705	calreticulin - bar
23	810.5	52.2	425	2 C96605	calreticulin (ctrl
24	801.5	51.6	444	2 H85224	hypothetical prote
25	643	41.4	622	2 S71342	calnexin precursor
26	633	40.8	591	2 B54354	calnexin precursor
27	629	40.5	591	2 C54354	calnexin precursor
28	628	40.4	592	2 I53260	calnexin - human
29	628	40.4	592	2 A45673	calnexin precursor

## RESULT 1

A37047

calreticulin precursor - human

N;Alternate names: 52K ribonucleoprotein autoantigen Ro/SS-A; 60K integrin-binding prote.  
C;Species: Homo sapiens (man)

C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 18-Feb-2000

C;Accession: A42330; A37047; A46452; A28812; PH1525; A40346; S11475; T45075

R;McCaulliffe, D.P.; Yang, Y.S.; Wilson, J.; Sontheimer, R.D.; Capra, J.D.

J. Biol. Chem. 267, 2557-2562, 1992

A;Title: The 5'-flanking region of the human calreticulin gene shares homology with the

A;Reference number: A42330; MUID:92129342; PMID:1731953

A;Accession: A42330

A;Molecule type: DNA

A;Residues: 1-417 cMC2>

A;Note: sequence extracted from NCBI backbone (NCBIN:78537, NCBI:78536)

R;McCaulliffe, D.P.; Lux, F.A.; Liew, T.S.; Sanz, I.; Hanke, J.; Newkirk, M.M.; Bachinski

J. Clin. Invest. 85, 1379-1391, 1990

A;Title: Molecular cloning, expression, and chromosome 19 localization of a human Ro/SS-

A;Reference number: A37047; MUID:90237213; PMID:2332496

A;Accession: A37047

A;Molecule type: mRNA

A;Residues: 1-417 cMCC>

A;Cross-references: GB:M32294; NID:g337486; PIDN:AAA36582.1; PID:g337487

A;Note: the authors translated the codon GTA for residue 349 as Tyr

R;Kokach, J.A.; Haseby, J.A.; Meilof, J.F.; Smeenk, R.J.; Umansh, T.R.; Greene, B.M.;

J. Immunol. 147, 3031-3039, 1991

A;Title: Characterization of the autoantigen calreticulin.

A;Reference number: A46452; MUID:92013129; PMID:1919005

A;Accession: A46452

A;Molecule type: mRNA

A;Residues: 1-417 cROK>

A;Cross-references: GB:M84739; NID:g179881; PIDN:AAA51916.1; PID:g179882

A;Note: sequence extracted from NCBI backbone (NCBIN:60749, NCBI:60750)

R;Lieu, T.S.; Newkirk, M.M.; Capra, J.D.; Sontheimer, R.D.

J. Clin. Invest. 82, 96-101, 1988

A;Title: Molecular characterization of human Ro/SS-A antigen. Amino terminal sequence of

A;Reference number: A28812; MUID:88273610; PMID:3260607

A;Accession: A28812

A;Molecule type: protein

A;Residues: 18-41 <LIE>

A;Note: 18-Ala was also found

R;Dupuis, M.; Schaefer, E.; Krause, K.H.; Tschopp, J.

J. Exp. Med. 177, 1-7, 1993

A;Title: The calcium-binding protein calreticulin is a major constituent of lytic granul

A;Reference number: PH1525; MUID:93115648; PMID:8418194

A;Accession: PH1525

A;Molecule type: protein

A;Residues: 18-27 <DUF>

A;Experimental source: LAX cell

R;Rojiani, M.V.; Finlay, S.B.; Gray, V.; Dedhar, S.

Biochemistry 30, 9859-9865, 1991

A;Title: In vitro interaction of a polypeptide homologous to human Ro/SS-A antigen (calr



R;Murthy, K.K.; Banville, D.; Srikant, C.B.; Carrier, F.; Holmes, C.; Bell, A.; Patel, Y.  
Nucleic Acids Res. 18, 4933, 1990  
A;Title: Structural homology between the rat calreticulin gene product and the Onchocerca  
A;Reference number: S11205; MUID:90370496; PMID:2395661  
A;Accession: S11205  
A;Molecule type: mRNA  
A;Residues: 1-416 <VR>  
A;Cross-references: EMBL:X53363; NID:955854; PIDN:CAA37446.1; PID:955855  
R;Nakamura, M.; Michikawa, Y.; Baba, T.; Okinaga, S.; Arai, K.  
Biochem. Biophys. Res. Commun. 186, 668-673, 1992  
A;Title: Calreticulin is present in the acrosome of spermatozoa of rat testis.  
A;Reference number: PC1109; MUID:92360010; PMID:1497655  
A;Accession: PC1109  
A;Molecule type: protein  
A;Residues: 18-32 <NAX>  
A;Experimental source: testis, strain Sprague-Dawley  
R;Soenichsen, B.; Fuellekrug, J.; van Nguyen, P.; Diekmann, W.; Robinson, D.G.; Mieskes  
submitted to the EMBL Data Library, May 1994  
A;Description: Retention and retrieval: both mechanisms cooperate to maintain calreticulin  
A;Reference number: S45036  
A;Accession: S45036  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-415 <SE>  
A;Cross-references: EMBL:X79327; NID:9488840; PIDN:CAA55890.1; PID:9488841  
R;Lone, Y.C.; Bailly, A.; Latruffe, N.  
submitted to the EMBL Data Library, December 1988  
A;Reference number: S04867  
A;Accession: S04867  
A;Molecule type: mRNA  
A;Residues: X' 270-358, 'RAG' <LON>  
A;Cross-references: EMBL:X13702; NID:956055; PIDN:CAA31987.1; PID:9390260  
A;Note: The authors designated the protein as D-beta-hydroxybutyrate dehydrogenase  
R;Yoko, T.; Nagayama, S.; Kajiwara, R.; Kawaguchi, Y.; Horiuchi, R.; Kamataki, T.  
Biochim. Biophys. Acta 1158, 339-344, 1993  
A;Title: Identification of protein disulfide isomerase and calreticulin as autoimmune an  
A;Reference number: S39371; MUID:94072621; PMID:8251535  
A;Accession: S39372  
A;Molecule type: protein  
A;Residues: 18-23, 'X', 25-32 <YOK>  
R;Van, P.N.; Peter, F.; Soeling, H.D.  
J. Biol. Chem. 264, 17494-17501, 1989  
A;Title: Four intracisternal calcium-binding glycoproteins from rat liver microsomes wit  
itive calcium sequestering rat liver vesicles.  
A;Reference number: A34473; MUID:90008920; PMID:2793869  
A;Accession: A34473  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 18-36 <VAN>  
R;Treves, S.; de Mattei, M.; Lanfredi, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; Meld  
Biochem. J. 271, 473-480, 1990  
A;Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-storage  
A;Reference number: S13045; MUID:91054414; PMID:2241926  
A;Accession: S13045  
A;Molecule type: protein  
A;Residues: 18-29 <TR>  
C;Superfamily: calreticulin  
C;Keywords: calcium binding; glycoprotein  
F;1-17/Domain: signal sequence #status predicted <SIG>  
F;18-416/Product: calreticulin #status experimental <MAT>  
F;204-212/Region: nuclear location signal  
F;413-416/Region: endoplasmic reticulum retention signal  
F;344/Binding site: carbonylate (Asn) (covalent) #status predicted  
Query Match 95.1%; Score 1476.5; DB 2; Length 416;  
Best Local Similarity 94.6%; Pred. No. 1.1e-82;  
Matches 265; Conservative 10; Mismatches 4; Indels 1; Gaps 1;  
QY 1 GPGTKVHVIFNYKGNVLINKIRCKDEFTHTLYTLVRPDNTYEVKIDNSQVESGSL 60  
DB 138 GPGTKVHVIFNYKGNVLINKIRCKDEFTHTLYTLVRPDNTYEVKIDNSQVESGSL 197  
QY 61 DDWDFLPKKIKDPASKEPDWDERAKIDDPDTSKPEDWDPKPEHIPDPDAKKPDWDEEM 120

DB 198 DDWDFLPKKIKDPASKEPDWDERAKIDDPDTSKPEDWDPKPEHIPDPDAKKPDWDEEM 257  
QY 121 DGEWEPVQNPYKGEWKPRQIDNPDKYKGTWIKTWHPEIDNPEYSPDPIYAYDNFVGLGD 180  
DB 258 DGEWEPVQNPYKGEWKPRQIDNPDKYKGTWIKTWHPEIDNPEYSPDPIYAYDSFAVLGLD 317  
QY 181 LMQVKSQGTIFDNFLITNDAYAEFGNETGWGTVAEKQMKDKQDEBQRLKEEEDKKRK 240  
DB 318 LMQVKSQGTIFDNFLITNDAYAEFGNETGWGTVAEKQMKDKQDEBQRLKEEEDKKRK 377  
QY 241 EEEEAEDKDE 280  
DB 378 EEEEAEDKDE 416  
RESULT 4  
A34154  
calreticulin precursor, skeletal muscle - rabbit  
C;Species: Oryctolagus cuniculus (domestic rabbit)  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C;Accession: A34154; S13047  
R;Fliegel, L.; Burns, K.; MacLennan, D.H.; Reithmeier, R.A.F.; Michalak, M.  
J. Biol. Chem. 264, 21522-21528, 1989  
A;Title: Molecular cloning of the high affinity calcium-binding protein (calreticulin) o  
A;Reference number: A34154; MUID:90094320; PMID:2600080  
A;Accession: A34154  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-418 <FLI>  
A;Cross-references: GB|J05138; NID:9164858; PIDN:AAA31188.1; PID:9164859  
R;Treves, S.; de Mattei, M.; Lanfredi, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; Meld  
Biochem. J. 271, 473-480, 1990  
A;Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-storage  
A;Reference number: S13045; MUID:91054414; PMID:2241926  
A;Accession: S13047  
A;Molecule type: protein  
A;Residues: 19-32 <TR>  
C;Superfamily: calreticulin  
C;Keywords: skeletal muscle  
F;1-17/Domain: signal sequence #status predicted <SIG>  
F;415-418/Region: endoplasmic reticulum retention signal  
Query Match 93.9%; Score 1457.5; DB 1; Length 418;  
Best Local Similarity 93.2%; Pred. No. 1.6e-81;  
Matches 282; Conservative 11; Mismatches 7; Indels 1; Gaps 1;  
QY 1 GPGTKVHVIFNYKGNVLINKIRCKDEFTHTLYTLVRPDNTYEVKIDNSQVESGSL 60  
DB 138 GPGTKVHVIFNYKGNVLINKIRCKDEFTHTLYTLVRPDNTYEVKIDNSQVESGSL 197  
QY 61 DDWDFLPKKIKDPASKEPDWDERAKIDDPDTSKPEDWDPKPEHIPDPDAKKPDWDEEM 120  
DB 198 DDWDFLPKKIKDPASKEPDWDERAKIDDPDTSKPEDWDPKPEHIPDPDAKKPDWDEEM 257  
QY 121 DGEWEPVQNPYKGEWKPRQIDNPDKYKGTWIKTWHPEIDNPEYSPDPIYAYDNFVGLGD 180  
DB 258 DGEWEPVQNPYKGEWKPRQIDNPDKYKGTWIKTWHPEIDNPEYSPDPIYAYDSFAVLGLD 317  
QY 181 LMQVKSQGTIFDNFLITNDAYAEFGNETGWGTVAEKQMKDKQDEBQRLKEEEDKKRK 240  
DB 318 LMQVKSQGTIFDNFLITNDAYAEFGNETGWGTVAEKQMKDKQDEBQRLKEEEDKKRK 377  
QY 241 EEEEA-EDKDE 280  
DB 378 EEEEAEDKDE 418  
RESULT 5  
S43376  
calreticulin, brain isoform 1 - bovine  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 20-Oct-1994 #sequence\_revision 23-Mar-1995 #text\_change 07-May-1999

```

F:193/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match          92.2%; Score 1432; DB 2; Length 421;
Best Local Similarity 92.2%; Pred. No. 5.7e-80;
Matches 259; Conservative 12; Mismatches 8; Indels 2; Gaps 2;

QY      1  GPGTKKVHVIENYKGNVLINKDIRCKDDFEFTHLYTLIVRPNTYEVKIDNSQVESGSLE 60
Db      142 GPGTKKVHVIENYKGNVLINKDIRCKDDFEFTHLYTLIVRPNTYEVKIDNSQVESGSLE 201

QY      61  DDWDFLPPKKIKDPDASKPEDWDERAKIDDPDTSKPEDWDPKEHIPDPDAKPPEDWDEEM 120
Db      202 DDWDFLPPKKIKDPDAAKPEDWDRAKIDDPDTSKPEDWDPKEHIPDPDAKPPEDWDEEM 261

QY      121 DGEWEPPIQNPEYKGEWKPRQIDNPDKYGTWTHPEIDNPSPDPPIYAYDNFVGLGLD 180
Db      262 DGEWEPPIQNPEYKGEWKPRQIDNPDKYGTWTHPEIDNPSPDPPIYAYDNFVGLGLD 321

QY      181 LWQVKSGTIFDNFLINTDEAYAEFGNETWGTVTKAAEKQMKQDDEQRLEKEEEDKKRK 240
Db      322 LWQVKSGTIFDNFLINTDEAYAEFGNETWGTVTKAAEKQMKQDDEQRLEHEEEKKRK 381

QY      241 EEEEAEDKEDDDKDEDEDEDEKDEDEED-VPGCAKDEL 280
Db      382 EEEEA-E-KDDDDKDEDEDEDEKDEEEEDAAAQAKDEL 421

RESULT 7
S29129
calreticulin precursor (clone 3) - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
C:Accession: S29129
R:Treves, S.; Zorzato, F.; Pozzan, T.
Biochem. J. 287, 579-581, 1992
A:Title: Identification of calreticulin isoforms in the central nervous system.
A:Reference number: S29129; MUID:93074997; PMID:1445218
A:Accession: S29129
A:Molecule type: mRNA
A:Residues: 1-411 <TRE>
A:Cross-references: EMBL:X67597; NID:G64608; PIDN:CAA47866.1; PID:G64609
C:Superfamily: calreticulin
C:Keywords: glycoprotein
F:1-12/Domain: signal sequence (fragment) #status predicted <SIG>
F:13-411/Product: calreticulin #status predicted <MAT>
F:408-411/Region: endoplasmic reticulum retention signal
F:339/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match          82.5%; Score 1280.5; DB 2; Length 411;
Best Local Similarity 80.1%; Pred. No. 8.6e-71;
Matches 225; Conservative 31; Mismatches 22; Indels 3; Gaps 2;

QY      1  GPGTKKVHVIENYKGNVLINKDIRCKDDFEFTHLYTLIVRPNTYEVKIDNSQVESGSLE 60
Db      133 GPGTKKVHVIENYKGNVLINKDIRCKDDSTHLYTLIVRPNTYEVKIDNSQVESGSLE 192

QY      61  DDWDFLPPKKIKDPDASKPEDWDERAKIDDPDTSKPEDWDPKEHIPDPDAKPPEDWDEEM 120
Db      193 DDWDFLPPKKIKDPAKPPEDWDERPKIDDDPKDDEKPPDWEKPEHIPDPDAKPPEDWDEEM 252

QY      121 DGEWEPPIQNPEYKGEWKPRQIDNPDKYGTWTHPEIDNPSPDPPIYAYDNFVGLGLD 180
Db      253 DGEWEPPIQNPEYKGEWKPRQIDNPDKYGTWTHPEIDNPSPDPPIYAYDNFVGLGLD 312

QY      181 LWQVKSGTIFDNFLINTDEAYAEFGNETWGTVTKAAEKQMKQDDEQRLEKEEEDKKRK 240
Db      313 LWQVKSGTIFDNFLINTDEHAEBYGNETWGTVTKAEBKQMKQDDEQRLEKEEEDKKRK 372

QY      241 EEE-EAEDKEDDDKDEDEDEDEKDEDEEDVPGCAKDEL 280
Db      373 EEEPEQDEEDDDDEBEKEEKEEEDDEEETP--LKDEL 411

```

```

RESULT 8
S29130
calreticulin (clone 8) - African clawed frog (fragment)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
C;Accession: S29130; T01068
R;Preves, S.; Zorzato, F.; Pozzan, T.
Biochem. J. 287, 579-581, 1992
A;Title: Identification of calreticulin isoforms in the central nervous system.
A;Reference number: S29129; MUID:93074997; PMID:1445218
A;Accession: S29130
A;Molecule type: mRNA
A;Residues: 1-384 <TR>
A;Cross-references: EMBL:X67598
A;Accession: T01068
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-339, 'XTGR' <TR>
A;Cross-references: EMBL:X67598; NID:G64610; PIDN:CAA47867.1; PID:G64611
A;Experimental source: CNS
C;Superfamily: calreticulin
C;Keywords: glycoprotein
F;381-384/Region: endoplasmic reticulum retention signal
F;316/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 80.5%; Score 1249.5; DB 2; Length 384;
Best Local Similarity 78.2%; Pred. No. 6.1e-69;
Matches 219; Conservative 30; Mismatches 26; Indels 5; Gaps 1;

QY 1 GPTTKVHVIFNYKGNVLINKDIRCKDETHLYTLIVRPDNTYEVKIDNSQVESGSL 60
DB 110 GPTTKVHVIFNYKGNVLINKDIRCKDETHLYTLIVRPDNTYEVKIDNSQVESGSL 169

QY 61 DWDDELPPKKIKDPDASKPEDWDERAKIDDDPTDSKPEDWDXPEHIPDPDAKKPEDWDEEM 120
DB 170 EDWDFLPKKIKDPDASKPEDWDERAKIDDDPTDSKPEDWDXPEHIPDPDAKKPEDWDEEM 229

QY 121 DGEWPPVITNPEYKGNKPRQIDNPYKGTWHPEDINPEYSPDPSIAYDNGVLGLD 180
DB 230 DGEWPPVITNPEYKGNKPRQIDNPYKGTWHPEDINPEYSPDPSIAYDNGVLGLD 289

QY 181 LMQVSGTIFDNLITNDEAYAEFGNETGWTKAAEKQMKDKODEEORLKEEEDKKRK 240
DB 290 LMQVSGTIFDNLITNDEAYAEFGNETGWTKAAEKQMKDKODEEORLKEEEDKKRK 349

QY 241 EEEAEKDEDDKDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 280
DB 350 EEEAEKDEDDKDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 384

RESULT 9
S71343
calreticulin precursor - Korean frog
C;Species: Rana rugosa (Korean frog)
C;Date: 29-Jan-1998 #sequence_revision 13-Feb-1998 #text_change 20-Jun-2000
C;Accession: S71343
R;Yamamoto, S.; Nakamura, M.
FEBS Lett. 387, 27-32, 1996
A;Title: Calnexin: its molecular cloning and expression in the liver of the frog, Rana
A;Reference number: S71342; MUID:96234004; PMID:8654561
A;Accession: S71343
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-419 <YAM>
A;Cross-references: EMBL:D78589; NID:g1514956; PIDN:BAAL1425.1; PID:g1514957
C;Superfamily: calreticulin
C;Keywords: calcium binding; endoplasmic reticulum
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-419/Product: calreticulin #status predicted <MAT>
F;205-213/Region: nuclear location signal
F;415-418/Region: endoplasmic reticulum retention signal

Query Match 79.9%; Score 1241.5; DB 2; Length 419;

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Best Local Similarity 76.9%; Pred. No. 2e-68;
Matches 216; Conservative 34; Mismatches 30; Indels 1; Gaps 1;

QY 1 GPTTKVHVIFNYKGNVLINKDIRCKDETHLYTLIVRPDNTYEVKIDNSQVESGSL 60
DB 139 GPTTKVHVIFNYKGNVLINKDIRKADVVSHLYTLIVRPDNTYEVKIDNSQVESGSL 198

QY 61 DWDDELPPKKIKDPDASKPEDWDERAKIDDDPTDSKPEDWDXPEHIPDPDAKKPEDWDEEM 120
DB 199 DWDDELPPKKIKDPDASKPEDWDERAKIDDDPTDSKPEDWDXPEHIPDPDAKKPEDWDEEM 258

QY 121 DGEWPPVITNPEYKGNKPRQIDNPYKGTWHPEDINPEYSPDPSIAYDNGVLGLD 180
DB 259 DGEWPPVITNPEYKGNKPRQIDNPYKGTWHPEDINPEYSPDPSIAYDNGVLGLD 318

QY 181 LMQVSGTIFDNLITNDEAYAEFGNETGWTKAAEKQMKDKODEEORLKEEEDKKRK 240
DB 319 LMQVSGTIFDNLITNDEAYAEFGNETGWTKAAEKQMKDKODEEORLKEEEDKKRK 378

QY 241 EEEAEKDEDDKDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 280
DB 379 EEEAEKDEDDKDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 419

RESULT 10
JH0795
calreticulin precursor - California sea hare
N;Alternate names: protein 407
C;Species: Aplysia californica (California sea hare)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: JH0795; B31409; F60977
R;Kennedy, T.E.; Kuhl, D.; Barzilai, A.; Sweatt, J.D.; Kandel, E.R.
Neuron 9, 1013-1024, 1992
A;Title: Long-term sensitization training in aplysia leads to an increase in calreticulin.
A;Reference number: JH0795; MUID:93098937; PMID:1463604
A;Accession: JH0795
A;Molecule type: mRNA
A;Residues: 1-405 <KEN>
A;Cross-references: GS:S1239; NID:9262053; PIDN:AAB24569.1; PID:9262054
A;Experimental source: abdominal ganglion and antral nervous system
R;Kennedy, T.E.; Gawinowicz, M.A.; Barzilai, A.; Kandel, E.R.; Sweatt, J.D.
Proc. Natl. Acad. Sci. U.S.A. 85, 7008-7012, 1988
A;Title: Sequencing of proteins from two-dimensional gels by using in situ digestion and
A;Reference number: A94207; MUID:88320566; PMID:3413132
A;Accession: B31409
A;Molecule type: protein
A;Residues: 'X', 17-28, 'X', 30-31 <KE2>
R;Sweatt, J.D.; Kennedy, T.E.; Wager-Smith, K.; Gawinowicz, M.A.; Barzilai, A.; Karl, K.
Electrophoresis 10, 152-157, 1989
A;Title: Development of a database of amino acid sequences for proteins identified and i
A;Reference number: A60977; MUID:89276264; PMID:2731514
A;Accession: F60977
A;Molecule type: protein
A;Residues: 'X', 17-28, 'X', 30-31 <SWE>
C;Superfamily: calreticulin
C;Keywords: calcium binding; endoplasmic reticulum
F;1-15/Domain: signal sequence #status predicted <SIG>
F;16-405/Product: calreticulin #status experimental <MAT>
F;402-405/Region: endoplasmic reticulum retention signal

Query Match 75.0%; Score 1164; DB 1; Length 405;
Best Local Similarity 72.9%; Pred. No. 9.9e-64;
Matches 204; Conservative 29; Mismatches 39; Indels 8; Gaps 2;

QY 1 GPTTKVHVIFNYKGNVLINKDIRCKDETHLYTLIVRPDNTYEVKIDNSQVESGSL 60
DB 134 GPTTKVHVIFNYKGNVLINKDIRCKDDVPSHLYTLIVRPDNTYEVKIDNEKAEAGSL 193

QY 61 DWDDELPPKKIKDPDASKPEDWDERAKIDDDPTDSKPEDWDXPEHIPDPDAKKPEDWDEEM 120
DB 194 ADWDFLPARTIPDPDAKKPEDWDERAKIDDDPTDSKPEDWDXPEHIPDPDAKKPEDWDEEM 253

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S25851

calreticulin precursor - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 06-Jan-1994 #sequence\_revision 10-Nov-1995 #text\_change 05-Nov-1999

C:Accession: S25851; T33996

R:Smith, M.J.

DNA Seq. 2, 235-240, 1992

A:Title: A. C. elegans gene encodes a protein homologous to mammalian calreticulin.

A:Reference number: S25851; MUID:92329978; PMID:1627827

A:Accession: S25851

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-395 <SMI>

A:Cross-references: EMBL:X59589; NID:g6693; PIDN:CAA42159.1; PID:g6694

R:Bauer, C.; Courtney, L.; Laplant, Y.

submitted to the EMBL Data Library, February 1999

A:Description: The sequence of C. elegans cosmid Y38A10A.

A:Reference number: Z21453

A:Accession: T33996

A>Status: preliminary; translated from GB/EMBL/DDBU

A:Molecule type: DNA

A:Residues: 1-395 <BAU>

A:Cross-references: EMBL:AF125963; PIDN:AAD14746.1; GSPDB:GNC0023; CESP:Y38A10A.5

A:Experimental source: strain Bristol N2; clone Y38A10A

C:Genetics:

A:Gene: CESP:Y38A10A.5

A:Map position: 5

A:Introns: 107/3; 315/3

C:Superfamily: calreticulin

F:1-15/Domain: signal sequence #status predicted <SIG>

F:392-395/Region: endoplasmic reticulum retention signal

Query Match 63.8%; Score 991.5; DB 2; Length 395;

Best Local Similarity 66.0%; Pred. No. 2.8e-53;

Matches 173; Conservative 35; Mismatches 53; Indels 1; Gaps 1;

Qy 1 GPQTKVHVIFNYKGNVLINKDIRCKDDEFFHLYTLIVRPDNTYEVKIDNSQVSGSLE 60

Db 134 GP-TRRVHVLNKGKGLIKKEITCKSDHLHLYTLILNSDNTYEVKIDGESAQTSLE 192

Qy 61 DWDVFLPPKIKDPPDASKEDWDERAKIDDPDTSKPEDWDKPEHIPDPDAKKPEDWDEM 120

Db 193 EDWDLPAKKIKDPPDAKKPEDWDEREYI DDAADAKPEDWEKPEHIPDPDAKKPEDWDEM 252

Qy 121 DGEWEPPIQNPEYKGEWPKPQLDNDPDKYKGTWHPEIDNPEYSPDPSIYAYDNFVGLGD 180

Db 253 DGEWEPMDINDPEYKGEWPKQIKKPAKYGKWIHPEINPEYTPDDELYSYSGAIGFD 312

Qy 181 LMQVKSQTTFDNLINDSAYAEFGNETPGWTKAAEKQMKDKDEQRLEKEEEDKKRK 240

Db 313 LMQVKSQTTFDNIITDSVEEAFAAAETFDKLTVEKEKEKADAEETRKAEERKKA 372

Qy 241 EEEAEKEDKEDDQKDEDEDEE 262

Db 373 EKEAKDDEEKEEKGHDE 394

RESULT 13

A32507

41K larval antigen - nematode (Onchocerca volvulus) (fragment)

C:Species: Onchocerca volvulus

C>Date: 21-May-1990 #sequence\_revision 21-May-1990 #text\_change 12-Apr-1995

C:Accession: A32507; A28813

R:Unnasch, T.R.; Gallin, M.Y.; Soboslay, P.T.; Erttmann, K.D.; Greene, B.M.

J. Clin. Invest. 82, 262-269, 1988

A:Title: Isolation and characterization of expression cDNA clones encoding antigens of

A:Reference number: A32769; MUID:89273584; PMID:2455736

A:Accession: A32507

A:Molecule type: mRNA

A:Residues: 1-336 <UNN>

C:Superfamily: calreticulin

Query Match 60.8%; Score 944.5; DB 2; Length 336;

[illegible]

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Db 139 GPTKKVHVIFQYKKKNLQINCKDQSFTHLYTLIVRPDNTYEVKIDNSKVESGSL 198  
 QY 61 DWDWFLPPKKIKDPDASKEDWDERAKIDDPDTSKPEDWKEPHIPDPDAKPEDWDEEM 120  
 Db 199 DWDWFLPPKKIKDPDASKEDWDERAKIDDPDTSKPEDWKEPHIPDPDAKPEDWDEEM 258  
 QY 121 DGEWEPVQNPYKGEWKPRQIDNPDKYGTWHPHIDNPYSPDPSIYAYDNFVGLD 180  
 Db 259 DGEWEPVQNPYKGEWKPRQIDNPDKYGTWHPHIDNPYSPDPSIYAYDNFVGLD 318  
 QY 181 LMQVSGTIFDNLITNDEAYAEFGNETGWTKAAEKQMKQDEORLKEEEDKKRK 240  
 Db 319 LMQVSGTIFDNLITNDEAYAEFGNETGWTKAAEKQMKQDEORLKEEEDKKRK 378  
 QY 241 EEE--EAEDKEDDEDKEDEEDKEDEEDVPGQAKDEL 280  
 Db 379 EEPQEEDEDDDDDEEKEEKEEKEEEDDEETP--LKDEL 418  
 RESULT 2  
 Q91710  
 ID Q91710 PRELIMINARY; PRT; 411 AA.  
 AC Q91710;  
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Calreticulin precursor (Fragment).  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=CNS;  
 RA Traves S, Zorzato F., Pozzan T.;  
 RT "Identification of calreticulin isoform in the CNS.";  
 RL Biochem. J. 0:0-0(0).  
 DR EMBL; X67597; CAA47866.1; -.  
 DR PIR; S29129; S29129.  
 DR GO; GO:0005514; F:calcium ion storage activity; IEA.  
 DR InterPro; IPR001580; Calreticulin.  
 DR InterPro; IPR003033; Calret. calnex P.  
 DR InterPro; IPR008985; ConA-like lec\_gi.  
 DR InterPro; IPR00886; ER target S.  
 DR Pfam; PF00262; calreticulin; 1.  
 DR PRINTS; PR00626; CALRETICULIN.  
 DR ProDom; PDC01866; Calreticulin; 1.  
 DR PROSITE; PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 2.  
 DR PROSITE; PS00014; ER\_TARGET; 1.  
 KW Signal.  
 FT NON TER 1 12 POTENTIAL.  
 FT SIGNAL <1 12 CALRETICULIN.  
 FT CHAIN 13 411  
 SQ SEQUENCE 411 AA; 49344 MW; 5910465008E8FA CRC64;  
 Query Match 82.5%; Score 1280.5; DB 13; Length 411;  
 Best Local Similarity 80.4%; Pred. No. 8.8e-79;  
 Matches 225; Conservative 31; Mismatches 22; Indels 3; Gaps 2;  
 QY 1 GPTKKVHVIFQYKKKNLQINCKDQSFTHLYTLIVRPDNTYEVKIDNSKVESGSL 60  
 Db 133 GPTKKVHVIFQYKKKNLQINCKDQSFTHLYTLIVRPDNTYEVKIDNSKVESGSL 192  
 QY 61 DWDWFLPPKKIKDPDASKEDWDERAKIDDPDTSKPEDWKEPHIPDPDAKPEDWDEEM 120  
 Db 193 DWDWFLPPKKIKDPDASKEDWDERAKIDDPDTSKPEDWKEPHIPDPDAKPEDWDEEM 252  
 QY 121 DGEWEPVQNPYKGEWKPRQIDNPDKYGTWHPHIDNPYSPDPSIYAYDNFVGLD 180  
 Db 253 DGEWEPVQNPYKGEWKPRQIDNPDKYGTWHPHIDNPYSPDPSIYAYDNFVGLD 312

QY 181 LMQVSGTIFDNLITNDEAYAEFGNETGWTKAAEKQMKQDEORLKEEEDKKRK 240  
 Db 313 LMQVSGTIFDNLITNDEAYAEFGNETGWTKAAEKQMKQDEORLKEEEDKKRK 372  
 QY 241 EEE--EAEDKEDDEDKEDEEDKEDEEDVPGQAKDEL 280  
 Db 373 EEPQEEDEDDDDDEEKEEKEEKEEEDDEETP--LKDEL 411  
 RESULT 3  
 Q7ZWU8  
 ID Q7ZWU8 PRELIMINARY; PRT; 413 AA.  
 AC Q7ZWU8;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Similar to calreticulin.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Embryo;  
 RA Klein S., Strausberg R.;  
 RL Submitted (Feb-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC046699; AAH46699.1; -.  
 DR GO; GO:0005514; F:calcium ion storage activity; IEA.  
 DR InterPro; IPR001580; Calreticulin.  
 DR InterPro; IPR009033; Calret. calnex P.  
 DR InterPro; IPR008985; ConA-like lec\_gi.  
 DR InterPro; IPR00886; ER target S.  
 DR Pfam; PF00262; calreticulin; 1.  
 DR PRINTS; PR00626; CALRETICULIN.  
 DR ProDom; PDC01866; Calreticulin; 1.  
 DR PROSITE; PS00803; CALRETICULIN\_1; 1.  
 DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.  
 DR PROSITE; PS00014; ER\_TARGET; 1.  
 SQ SEQUENCE 413 AA; 48521 MW; DE002F8F0523772B CRC64;  
 Query Match 81.2%; Score 1261.5; DB 13; Length 413;  
 Best Local Similarity 78.9%; Pred. No. 1.7e-77;  
 Matches 221; Conservative 29; Mismatches 25; Indels 5; Gaps 1;  
 QY 1 GPTKKVHVIFQYKKKNLQINCKDQSFTHLYTLIVRPDNTYEVKIDNSKVESGSL 60  
 Db 139 GPTKKVHVIFQYKKKNLQINCKDQSFTHLYTLIVRPDNTYEVKIDNSKVESGSL 198  
 QY 61 DWDWFLPPKKIKDPDASKEDWDERAKIDDPDTSKPEDWKEPHIPDPDAKPEDWDEEM 120  
 Db 199 DWDWFLPPKKIKDPDASKEDWDERAKIDDPDTSKPEDWKEPHIPDPDAKPEDWDEEM 258  
 QY 121 DGEWEPVQNPYKGEWKPRQIDNPDKYGTWHPHIDNPYSPDPSIYAYDNFVGLD 180  
 Db 259 DGEWEPVQNPYKGEWKPRQIDNPDKYGTWHPHIDNPYSPDPSIYAYDNFVGLD 318  
 QY 181 LMQVSGTIFDNLITNDEAYAEFGNETGWTKAAEKQMKQDEORLKEEEDKKRK 240  
 Db 319 LMQVSGTIFDNLITNDEAYAEFGNETGWTKAAEKQMKQDEORLKEEEDKKRK 378  
 QY 241 EEE--EAEDKEDDEDKEDEEDKEDEEDVPGQAKDEL 280  
 Db 379 EEPQEEDEDDDDDEEKEEKEEKEEEDDEETP--LKDEL 413  
 RESULT 4  
 Q98984  
 ID Q98984 PRELIMINARY; PRT; 419 AA.  
 AC Q98984;  
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)

01-FEB-1997 (T-EMBLrel. 02, Last sequence update)  
01-OCT-2003 (T-EMBLrel. 25, Last annotation update)  
Calreticulin.  
Rana rugosa (Wrinkled frog).  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.  
NCBI\_TaxID=8410;  
[1]  
SEQUENCE FROM N.A.  
MEDLINE=96234004; PubMed=8654561;  
Yanamoto S.; Nakamura M.;  
"Calnexin: its molecular cloning and expression in the liver of the  
frog, Rana rugosa."  
FEBS Lett. 387:27-32(1996).  
[2]  
SEQUENCE FROM N.A.  
MEDLINE=96387817; PubMed=8795287;  
Yanamoto S.; Kondo Y.; Hanada H.; Nakamura M.;  
"Strong expression of the calreticulin gene in the liver of Rana  
rugosa tadpoles, but not adult frogs."  
J. Exp. Zool. 275:431-443(1996).  
[3]  
EMBL; D78589; BAAL1425.1; -.  
PIR; S71343; S71343.  
GO; GO:0005514; F:calcium ion storage activity; IEA.  
InterPro; IPR001580; Calreticulin.  
InterPro; IPR009033; Calreticulin.  
InterPro; IPR008985; ConA\_like\_lac\_gi.  
InterPro; IPR000886; ER\_target\_S.  
Pfam; PF00262; calreticulin; 1.  
PRINTS; P00626; CALRETICULIN.  
ProDom; PD001866; Calreticulin; 1.  
PROSITE; PS00803; CALRETICULIN\_1; 1.  
PROSITE; PS00804; CALRETICULIN\_2; 1.  
PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.  
PROSITE; PS00014; ER\_TARGET; 1.  
SEQUENCE 419 AA; 48658 MW; 2C857036769673BF CRC64;  
SQ

Query Match 79.9%; Score 1241.5; DB 13; Length 419;  
Best Local Similarity 76.9%; Pred. No. 3.8e-76;  
Matches 216; Conservative 34; Mismatches 30; Indels 1; Gaps 1;  
QY 1 GPGTKKVVHVFYNYKGNVLINKDIRKDDPETHLYTLIVRPDNTVEYKIDNSQVSGSLE 60  
DB 139 GPTTKKVVHVFYNYKGNVLINKDIRKDDPETHLYTLIVRPDNTVEYKIDNSQVSGSLE 198  
QY 61 DWDWFLPPKKIKDPASKEPDWDERAKIDDDPDSKPEDWKEHIPPDPDAKPPEDWDEEM 120  
DB 199 DWDWFLPPKKIKDPASKEPDWDERAKIDDDPDSKPEDWKEHIPPDPDAKPPEDWDEEM 258  
QY 121 DGEWEPPIVTONPEYKGEWKPRQIDNPDKYKGTWGHPEIDNPPEYSPDIYAYDNFVGLD 180  
DB 259 DGEWEPPIVTONPEYKGEWKPRQIDNPDKYKGTWGHPEIDNPPEYSPDIYAYDNFVGLD 318  
QY 181 LWOVKSGLTIFDNLITNDAYAEFGNETGWTKAABKQKQDEEQLKKEEEDKKRK 240  
DB 319 LWOVKSGLTIFDNLITDDKFAEEHATKWTGVTKEGKQKQDEEERKQDEEERKKRK 378  
QY 241 EEEAEADKDDKDEDEDEE-DEEEDVPGQAKDEL 280  
DB 379 EOEPAEASDDDDDDDDDEEKEKEEEDVPGQAKDEL 419

RESULT 5  
Q7SZM3 PRELIMINARY; PRT; 423 AA.  
AC Q7SZM3;  
DT 01-OCT-2003 (T-EMBLrel. 25, Created)  
DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)  
DE ER-resident chaperone calreticulin.  
OS Ictalurus punctatus (Channel catfish).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;

OC Ictaluridae; Ictalurus.  
OX NCBI\_TaxID=7998;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA McConnell T.J.; Pitzer J.E.;  
RT "Calreticulin in the Channel Catfish, Ictalurus punctatus."  
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY342298; AAQ19852.1; -.  
SQ SEQUENCE 423 AA; 49186 MW; ED7CBA5C1FBC07EB CRC64;  
Query Match 77.1%; Score 1198; DB 13; Length 423;  
Best Local Similarity 73.7%; Pred. No. 3.3e-73;  
Matches 213; Conservative 36; Mismatches 28; Indels 12; Gaps 3;  
QY 1 GPGTKKVVHVFYNYKGNVLINKDIRKDDPETHLYTLIVRPDNTVEYKIDNSQVSGSLE 60  
DB 138 GPTTKKVVHVFYNYKGNVLINKDIRKDDPETHLYTLIVRPDNTVEYKIDNSQVSGSLE 197  
QY 61 DWDWFLPPKKIKDPASKEPDWDERAKIDDDPDSKPEDWKEHIPPDPDAKPPEDWDEEM 120  
DB 198 DWDWFLPPKKIKDPASKEPDWDERAKIDDDPDSKPEDWKEHIPPDPDAKPPEDWDEEM 257  
QY 121 DGEWEPPIVTONPEYKGEWKPRQIDNPDKYKGTWGHPEIDNPPEYSPDIYAYDNFVGLD 180  
DB 258 DGEWEPPIVTONPEYKGEWKPRQIDNPDKYKGTWGHPEIDNPPEYSPDIYAYDNFVGLD 317  
QY 181 LWOVKSGLTIFDNLITNDAYAEFGNETGWTKAABKQKQDEEQLKKEEEDKKRK 240  
DB 318 LWOVKSGLTIFDNLITDDKFAEEHATKWTGVTKEGKQKQDEEERKQDEEERKKRK 376  
QY 241 EEEAEADKDDKDEDEDEE-DEEEDVPGQAKDEL 280  
DB 377 KESEGEDEDDDEPEDEEEDVPGQAKDEL 423

RESULT 6  
Q9PTX7 PRELIMINARY; PRT; 318 AA.  
AC Q9PTX7;  
DT 01-MAY-2000 (T-EMBLrel. 13, Created)  
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)  
DE Calreticulin (fragment).  
OS Lampetra reissneri (Far Eastern brook lamprey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;  
OC Petromyzontiformes; Petromyzontidae; Lethenteron.  
OX NCBI\_TaxID=7753;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=10594174;  
RA Kuraku S.; Hoshiyama D.; Katoh K.; Suga H.; Miyata T.;  
RT "Monophyly of lampreys and hagfishes supported by nuclear DNA-coded  
genes."  
J. Mol. Evol. 49:729-735(1999).  
RL EMBL; AB025328; BAA88481.1; -.  
DR GO; GO:000514; F:calcium ion storage activity; IEA.  
DR InterPro; IPR001580; Calreticulin.  
DR InterPro; IPR009033; Calreticulin.  
DR InterPro; IPR008985; ConA\_like\_lac\_gi.  
DR InterPro; IPR000886; ER\_target\_S.  
DR Pfam; PF00262; calreticulin; 1.  
DR PRINTS; P00626; CALRETICULIN.  
DR ProDom; PD001866; Calreticulin; 1.  
DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.  
DR PROSITE; PS00014; ER\_TARGET; 1.  
FT NON TER 1  
SQ SEQUENCE 318 AA; 36997 MW; C88102EA1CAC1506 CRC64;

Query Match 76.2%; Score 1184; DB 13; Length 318;  
Best Local Similarity 73.1%; Pred. No. 2.2e-72;  
Matches 207; Conservative 36; Mismatches 36; Indels 4; Gaps 2;



[illegible][illegible]



DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT -01-JAN-1999 (TrEMBLrel. 09, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Calreticulin.  
 GN CRT-1.  
 OS Amblyomma americanum.  
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;  
 OC Parasitiformes; Ixodida; Ixodidae; Amblyomma.  
 OC NCBI\_TaxID=6943;  
 RN [1]  
 RP SEQUENCE OF 49-410 FROM N.A.  
 RC TISSUE=Salivary gland;  
 RA Jaworski D.C.; Simmen P.A.; Lamoreaux W.J.; Coons L.B.; Muller M.T.;  
 RA Needham G.R.;  
 RT "A secreted calreticulin protein in Ixodid tick (Amblyomma americanum)  
 RT saliva.";  
 RL J. Insect Physiol. 41:369-375(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Salivary gland;  
 RA Jaworski D.C.;  
 RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Salivary gland;  
 RA Fain-Thornton J.M.; Jaworski D.C.; Needham G.R.;  
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U07708; AAC79094.1; -.  
 DR GO; GO:0005514; F:calcium ion storage activity; IEA.  
 DR InterPro; IPR001580; Calreticulin.  
 DR InterPro; IPR009033; Calret calnex P.  
 DR InterPro; IPR008985; ConA like lec\_gl.  
 DR InterPro; IPR008986; ER target\_S.  
 DR Pfam; PF00262; calreticulin; 1.  
 DR PRINTS; PR00626; calreticulin; 1.  
 DR PROSITE; PS00805; CALRETICULIN; 1.  
 DR PROSITE; PS00804; CALRETICULIN\_2; 1.  
 DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.  
 DR PROSITE; PS00014; ER\_TARGET; 1.  
 DR PROSITE; PS00014; ER\_TARGET; 1.  
 DR SIGNAL.  
 KW SIGNAL.  
 FT CHAIN 1 19 POTENTIAL.  
 FT CHAIN 20 421 CALRETICULIN.  
 SQ SEQUENCE 421 AA; 48822 MW; 172C664F59F41P93 CRC64;  
 Query Match 70.4%; Score 1093.5; DB 5; Length 410;  
 Best Local Similarity 69.5%; Pred. No. 3.6e-66;  
 Matches 194; Conservative 25; Mismatches 49; Indels 11; Gaps 2;  
 QY 1 GPGTKKVVHVFNYKGNVLINKIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 60  
 DB 137 GPGTKKVVHVFNYKGNVLINKIRCKDDEFTHTLYTLIVKPDNTYVVKIDNEVAEKGELE 196  
 QY 61 DDWDFLPPKKIKDPDASKPEDWDERAKIDDPDTSKPEDWDXPEHIPDDPAKPEDWDEEM 120  
 DB 197 SDWSFLPPKKIKDPDASKPEDWDERAKIDDPDTSKPEDWDXPEHIPDDPAKPEDWDDM 256  
 QY 121 DGEWEPPTONPEYKGEWKPRQIDNPYKGTWTHPEIDNPESPDPSIYAYDNFVGLGLD 180  
 DB 257 DGEWEPPTONPEYKGEWKPRQIDNPYKGTWTHPEIDNPESPDPSIYAYDNFVGLGLD 316  
 QY 181 LWQVKSGLTFDNLITNDAYAEFGNETGWVTKAAEKQKMDQDEORLKEEEDKKRK 240  
 DB 317 LWQVKSGLTFDNLITDDDEYARVHGEETWAALKDEEKKKEKQ-----EEEDAKSK 369  
 QY 241 EEEAEDEKDE 279  
 DB 370 KEDDAK-----DEDEFEDEKEDEKEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 404  
 RESULT 15  
 Q9U6S0 PRELIMINARY; PRT; 421 AA.  
 AC Q9U6S0;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Calreticulin precursor.  
 GN CALRET.  
 OS Strongylocentrotus purpuratus (Purple sea urchin).  
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
 OC Echinoidea; Euechinoidea; Echinacea; Echinacea; Echinacea; Strongylocentrotidae;  
 OC Strongylocentrotus.  
 OC NCBI\_TaxID=7668;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Susan J.M.; Just M.L.; Lennarz W.J.;  
 RT "Cloning and Characterization of AlphaP Integrin and Calreticulin in  
 RT Embryos of the Sea Urchin.";  
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF177915; RAD55725.1; -.  
 DR GO; GO:0005514; F:calcium ion storage activity; IEA.  
 DR InterPro; IPR001580; Calreticulin.  
 DR InterPro; IPR009033; Calret calnex P.  
 DR InterPro; IPR008985; ConA like lec\_gl.  
 DR InterPro; IPR008986; ER target\_S.  
 DR Pfam; PF00262; calreticulin; 1.  
 DR PRINTS; PR00626; CALRETICULIN.  
 DR PROSITE; PS00804; CALRETICULIN; 1.  
 DR PROSITE; PS00805; CALRETICULIN\_2; 1.  
 DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 3.  
 DR PROSITE; PS00014; ER\_TARGET; 1.  
 DR PROSITE; PS00014; ER\_TARGET; 1.  
 DR SIGNAL.  
 KW SIGNAL.  
 FT CHAIN 1 19 POTENTIAL.  
 FT CHAIN 20 421 CALRETICULIN.  
 SQ SEQUENCE 421 AA; 48822 MW; 172C664F59F41P93 CRC64;  
 Query Match 67.6%; Score 1049.5; DB 5; Length 421;  
 Best Local Similarity 64.2%; Pred. No. 3.5e-63;  
 Matches 185; Conservative 47; Mismatches 45; Indels 11; Gaps 3;  
 QY 1 GPGTKKVVHVFNYKGNVLINKIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 60  
 DB 137 GPGTKKVVHVFNYKGNVLINKIRCKDDEFTHTLYTLIVKSDNSYEVRIIDNEKAQAGNLE 196  
 QY 61 DDWDFLPPKKIKDPDASKPEDWDERAKIDDPDTSKPEDWDXPEHIPDDPAKPEDWDEEM 120  
 DB 197 EDWDFLPSKMIKDPDASKPEDWDERAKIDDPDTSKPEDWDXPEHIPDDPAKPEDWDDM 256  
 QY 121 DGEWEPPTONPEYKGEWKPRQIDNPYKGTWTHPEIDNPESPDPSIYAYDNFVGLGLD 180  
 DB 257 DGEWEPPTONPEYKGEWKPRQIDNPYKGTWTHPEIDNPESPDPSIYAYDNFVGLGLD 316  
 QY 181 LWQVKSGLTFDNLITNDAYAEFGNETGWVTKAAEKQKMDQDEORLKEEEDKKRK 240  
 DB 317 LWQVKSGLTFDNLITDDLEAEKQAKLFVTKAAEKQKMDQDEAEERKQEEEDKKRK 376  
 QY 241 EE--EEAEKDEKDE 280  
 DB 377 EGGDE 421  
 Search completed: October 12, 2004, 15:47:23  
 Job time : 41 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 12, 2004, 15:46:05 ; Search time 13 Seconds  
(without alignments)  
1121.511 Million cell updates/sec

Title: US-09-807-148-9

Perfect score: 1553  
Sequence: 1 GPCTKXVHVIFNYKGNVLI.....EDXKDEEDVFGQAKDEL 280

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1553	100.0	417	CRTC_HUMAN	P27797 homo sapien
2	1490	95.9	417	CRTC_CRIGR	Q8K3H7 cricetus
3	1487.5	95.8	416	CRTC_MOUSE	P14211 mus musculus
4	1476.5	95.1	416	CRTC_RAT	P18418 rattus norv
5	1457.5	93.9	418	CRTC_RABIT	P15253 oryctolagus
6	1442	92.9	417	CRTL_BOVIN	P52193 bos taurus
7	1432	92.2	421	CRTL_BOVIN	P42918 bos taurus
8	1031.5	66.4	406	CRTC_DROME	P29413 drosophila
9	991.5	63.8	395	CRTC_CAEEL	P27798 caenorhabdi
10	944.5	60.8	388	RALI_ONCVO	P11012 onchocerca
11	856.5	55.2	415	CRTC_RICCO	P93508 ricinus com
12	837.5	53.9	420	CRTC_CHLSE	Q98td3 chlamydomon
13	837.5	53.9	420	CRTC_MAIZE	Q98p22 zea mays (m
14	824	53.1	424	CRTC_ARATH	Q38858 arabidopsis
15	821.5	52.9	421	CRTC_PRUAR	Q9xf98 prunus arme
16	818.5	52.7	416	CRTC_NICPL	Q40401 nicotiana p
17	817.5	52.6	393	CRTC_SCHMA	Q06814 schistosoma
18	814.5	52.4	416	CRTC_BETUV	Q08191 beta vulgar
19	810.5	52.2	425	CRTL_ARATH	O04151 arabidopsis
20	795	51.2	401	CRTC_EUGGR	Q9zny3 euglena gra
21	790.5	50.9	416	CRTC_BERST	Q92ppl berberis st
22	779	50.2	424	CRTC_ORYSA	Q9sly8 oryza sativ
23	764	49.2	424	CRTC_DICDI	Q23858 dictyosteli
24	699.5	45.0	424	CRTC_ARATH	O04153 arabidopsis
25	633	40.8	591	CALX_MOUSE	P35564 mus musculus
26	629	40.5	591	CALX_RAT	P35565 rattus norv
27	628	40.4	592	CALX_HUMAN	P27824 homo sapien
28	624	40.2	593	CALX_CANFA	P24643 canis famil
29	577.5	37.2	610	CALG_HUMAN	O14967 homo sapien
30	562.5	36.2	384	CRTC_HUMAN	Q96112 homo sapien
31	554	35.7	611	CALG_MOUSE	P52194 mus musculus
32	531	34.2	546	CALX_SOYEN	Q39817 glycine max
33	527	33.9	380	CRTC_MOUSE	Q949q6 mus musculus

ALIGNMENTS

RESULT 1

ID	CRTC_HUMAN	STANDARD;	PRT;	417 AA.
AC	P27797;			
DT	01-AUG-1992 (Rel. 23, Created)			
DT	01-AUG-1992 (Rel. 23, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Calreticulin precursor (CRP55) (Calregulin) (HACBP) (ERP60).			
GN	CALR OR CRTC.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=92013129; PubMed=1919005;			
RA	Rokeach L.A., Hasselby J.A., Meilof J.F., Smeenk R.J., Unnasch T.R.,			
RA	Greene B.M., Hoch S.O.;			
RT	"Characterization of the autoantigen calreticulin.";			
RL	J. Immunol. 147:3031-3039(1991).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=90237213; PubMed=2332496;			
RA	McCaulliffe D.P., Lux F.A., Lieu T.S., Sanz I., Hanke J., Newkirk M.M.,			
RA	Bachinski J.L., Itch Y., Siciliano M.J., Reichlin M., Sontheimer R.D.,			
RA	Capra J.D.;			
RT	"Molecular cloning, expression, and chromosome 19 localization of a			
RT	human Ro/SS-A autoantigen.";			
RL	J. Clin. Invest. 85:1379-1391(1990).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=92129342; PubMed=1733953;			
RA	McCaulliffe D.P., Yang Y.S., Wilson J., Sontheimer R.D., Capra J.D.;			
RT	"The 5'-flanking region of the human calreticulin gene shares			
RT	homology with the human GRP78, GRP94, and protein disulfide isomerase			
RT	promoters.";			
RL	J. Biol. Chem. 267:2557-2562(1992).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RA	Liu J., Peng X., Yuan J., Qiang B.;			
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RA	Lamerdin J.E., McCready P.M., Stilwagen S., Ramirez M., Carrano A.;			
RT	"Characterization by genomic sequence analysis of a gene-rich 111 kb			
RT	region of 19p13.2 containing the human DNA repair gene, RAD23A.";			
RL	Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.			
RN	[6]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Eye, Pancreas, and Skin;			
RX	MEDLINE=22398257; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			

P29402 arabidopsis  
O82709 pisum sativ  
Q35798 arabidopsis  
P35581 schizosach  
P34652 caenorhabdi  
Q39994 helianthus  
P27825 saccharomyc  
P08199 mesocricetu  
P91753 lytechinus  
P22620 plasmodium  
P09405 mus musculu  
P15771 gallus gall

34 501.5 32.3 530 1 CALX\_ARATH  
35 493 31.7 531 1 CALX\_BEA  
36 477.5 30.7 532 1 CALX\_ARATH  
37 472.5 30.4 560 1 CALX\_SCHPO  
38 472.5 30.4 619 1 CALX\_CAEEL  
39 451.5 29.1 540 1 CALX\_HELTU  
40 299.5 19.3 502 1 CALX\_YEAST  
41 184.5 11.9 713 1 NUCLE\_MESAU  
42 184 11.8 411 1 M962\_LYTPU  
43 183.5 11.8 743 1 ABRA\_PLASC  
44 177.5 11.4 706 1 NUCLE\_MOUSE  
45 176 11.3 694 1 NUCLE\_CHICK

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettunen M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length  
RL human and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [7]  
RP SEQUENCE OF 18-36.  
RX MEDLINE=9202034; PubMed=1911778;  
RA Rojiani M.V., Finlay B.B., Gray V., Dedhar S.;  
RT "In vitro interaction of a polypeptide homologous to human Ro/SS-A  
RT antigen (calreticulin) with a highly conserved amino acid sequence in  
RT the cytoplasmic domain of integrin alpha subunits.";  
RL Biochemistry 30:9859-9866 (1991).  
RN [8]  
RP SEQUENCE OF 18-32.  
RX MEDLINE=90380058; PubMed=2400400;  
RA Krause K.H., Simmerman H.K.B., Jones L.R., Campbell K.P.;  
RT "Sequence similarity of calreticulin with a Ca2(+)-binding protein  
RT that co-purifies with an Ins(1,4,5)P3-sensitive Ca2+ store in HL-60  
RT cells";  
RL Biochem. J. 270:545-548 (1990).  
RN [9]  
RP SEQUENCE OF 18-28.  
RC TISSUE=Liver.  
RX MEDLINE=93162045; PubMed=1286669;  
RA Hochstrasser D.F., Frutiger S., Paquet N., Bairoch A., Ravier F.,  
RA Pasquali C., Sanchez J.-C., Tissot J.-D., Bjellqvist B., Vargas R.,  
RA Appel R.D., Hughes G.J.;  
RT "Human liver protein map: a reference database established by  
RT microsequencing and gel comparison";  
RL Electrophoresis 13:992-1001 (1992).  
RN [10]  
RP PARTIAL SEQUENCE OF 25-34; 56-62; 208-221 AND 273-278.  
RC TISSUE=Keratinocytes;  
RX MEDLINE=93162043; PubMed=1286667;  
RA Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,  
RA Vandekerckhove J.;  
RT "Microsequences of 145 proteins recorded in the two-dimensional gel  
RT protein database of normal human epidermal keratinocytes";  
RL Electrophoresis 13:960-969 (1992).  
RN [11]  
RP SEQUENCE OF 18-26.  
RC TISSUE=Colon carcinoma;  
RX MEDLINE=97295305; PubMed=9150948;  
RA Ji H., Reid G.E., Moritz R.L., Eddes J.S., Burgess A.W., Simpson R.J.;  
RT "A two-dimensional gel database of human colon carcinoma proteins";  
RL Electrophoresis 18:605-613 (1997).  
CC -|- FUNCTION: This protein binds calcium. There are both high and low  
CC affinity calcium-binding sites.  
CC -|- SUBUNIT: Monomer (By similarity).  
CC -|- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.  
CC -|- SIMILARITY: Belongs to the calreticulin family.  
CC -|- CAUTION: Was originally (Ref.2) thought to be the 52 kDa Ro  
CC autoantigen.  
CC  
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DR EMBL; M84739; AAA51916.1; -;  
DR EMBL; M32294; AAA36582.1; -;  
DR EMBL; AY047586; AAL13126.1; -;  
DR EMBL; AD000092; AAB51176.1; -;  
DR EMBL; BC002500; AAH02500.1; -;  
DR EMBL; BC007911; AAH07911.1; -;  
DR EMBL; BC020493; AAH20493.1; -;  
DR PIR; A42330; A37047.  
DR PDB; 2CLR; 31-MAR-95.  
DR SWISS-2DPAGE; P27797; HUMAN  
DR Aarbus/Ghest-2DPAGE; 9401; IEP.  
DR HSC-2DPAGE; P27797; HUMAN.  
DR PHCI-2DPAGE; P27797; -;  
DR PMMA-2DPAGE; P27797; -;  
DR Siena-2DPAGE; P27797; -;  
DR Genew; HGNC:1455; CALR.  
DR MIM; 109091; -;  
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; TAS.  
DR InterPro; IPR009033; Calret\_cainex\_P.  
DR InterPro; IPR001880; Calreticulin.  
DR InterPro; IPR008985; ConA-like lec.gl.  
DR InterPro; IPR000886; ER target S.  
DR Pfam; PF00262; calreticulin; 1.  
DR PIRSF; PIRSF002356; Calreticulin; 1.  
DR PRINTS; PR00626; CALRETICULIN.  
DR Prodom; PD001866; Calreticulin; 1.  
DR PROSITE; PS00014; ER TARGET; 1.  
DR PROSITE; PS00803; CALRETICULIN 1; 1.  
DR PROSITE; PS00804; CALRETICULIN 2; 1.  
DR PROSITE; PS00805; CALRETICULIN REPEAT; 3.  
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal; 3D-structure.  
FT SIGNAL 1 17  
FT CHAIN 18 417  
FT DOMAIN 18 197  
FT DOMAIN 198 308  
FT DOMAIN 309 417  
FT DOMAIN 191 255  
FT REPEAT 191 202  
FT REPEAT 210 221  
FT REPEAT 227 238  
FT REPEAT 244 255  
FT DOMAIN 259 297  
FT REPEAT 259 269  
FT REPEAT 273 283  
FT REPEAT 287 297  
FT DOMAIN 351 408  
FT DISULFID 137 163  
FT SITE 414 417  
FT CONFLICT 35 35  
FT SEQUENCE 417 AA; 48141 MW; BC37C3CF1054FB2 CRC64;  
SQ  
Query Match 100.0%; Score 1553; DB 1; Length 417;  
Best Local Similarity 100.0%; Pred. No. 2.3e-84;  
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GPGTKKHVHIFNYKGVKLVINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSL 60  
DB 138 GPGTKKHVHIFNYKGVKLVINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSL 197  
QY 61 DDWDFLPKKIKDPDASKPDWDERAKIDDPDTSKPDWDKPEHI PDPDAKKPDWDDEEM 120  
DB 198 DDWDFLPKKIKDPDASKPDWDERAKIDDPDTSKPDWDKPEHI PDPDAKKPDWDDEEM 257  
QY 121 DGEWEPVIONPEYKGVKLVINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSL 180  
DB 258 DGEWEPVIONPEYKGVKLVINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSL 317  
QY 181 LQWQKSTIFDNLITNDEYAEFGNETGVTAAPKQMKDKQDEEQRKEEEDKKRK 240  
DB 318 LQWQKSTIFDNLITNDEYAEFGNETGVTAAPKQMKDKQDEEQRKEEEDKKRK 377  
QY 241 EEEAEDEKDE 280



[illegible]

\_\_\_\_\_



[illegible]

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RESULT 7
CRT2 BOVIN
ID CRT2 BOVIN STANDARD; PRT; 421 AA.
AC P42918;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Calreticulin brain isoform 2 precursor (CRP55) (Calregulin) (HACBP).
OS Bos taurus (Bovine); Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Catartiodactyla; Ruminantia; Pecora; Bovoidae;
OC Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
RX (1)
RN SEQUENCE FROM RP.
RT TISSUE=Brain;
RC MEDLINE=93385184; PubMed=8373827;
RA Liu N., Fine R.F., Johnson R.J.;
RX "Comparison of cDNAs from bovine brain coding for two isoforms of
RT calreticulin.";
RT Biochim. Biophys. Acta 1202:70-76(1993).
CC -!- FUNCTION: This protein binds calcium. There are both high and low
CC affinity calcium-binding sites.
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -!- SIMILARITY: Belongs to the calreticulin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collabora-
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CC entialises requires a license agreement (See http://www.isb-sib.ch/anno
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L13462; AAC37307.1; -.
CC PIR; S36799; S36799.
CC InterPro; IPR009033; Calret_calmex_P.
CC InterPro; IPR004580; Calreticulin.
CC InterPro; IPR009885; ConA_like Lec_gl.
CC InterPro; IPR000886; ER_target_S.
CC Pfam; PF00262; calreticulin; 1.
CC PIRSF; PIRSF002356; Calreticulin; 1.
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DR	PRINTS; PRO0626; CALRETICULIN.
DR	ProDom; PD001866; Calreticulin; 1.
DR	PROSITE; PS00014; ER TARGET; 1.
DR	PROSITE; PS00803; CALRETICULIN 1; 1.
DR	PROSITE; PS00804; CALRETICULIN 2; 1.
DR	PROSITE; PS00805; CALRETICULIN REPEAT; 3.
KW	Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT	SIGNAL 1 34 POTENTIAL
FT	CHAIN 35 421 CALRETICULIN, BRAIN ISOFORM 2.
FT	DOMAIN 35 201 N-DOMAIN.
FT	DOMAIN 202 312 C-DOMAIN.
FT	DOMAIN 313 421 C-DOMAIN.
FT	DOMAIN 195 259 4 X APPROXIMATE REPEATS.
FT	REPEAT 195 206 1-1.
FT	REPEAT 214 225 1-2.
FT	REPEAT 231 242 1-3.
FT	REPEAT 248 259 1-4.
FT	DOMAIN 263 301 3 X APPROXIMATE REPEATS.
FT	REPEAT 263 273 2-1.
FT	REPEAT 277 287 2-2.
FT	REPEAT 291 301 2-3.
FT	DOMAIN 366 411 ASP/GLU/LYS-RICH.
FT	DISULFID 141 167 BY SIMILARITY.
FT	CARBOHYD 163 183 N-LINKED (GLCNAC... ) (POTENTIAL).
FT	SITE 418 421 PREVENT SECRETION FROM ER.
SQ	SEQUENCE 421 AA; 48812 MW; 0257E959F7528BC CRC64;
Query Match 92.2%; Score 1432; DB 1; Length 421;	
Best Local Similarity 92.2%; Pred. No. 2.8e-77;	
Matches 259; Conservative 12; Mismatches 8; Indels 2; Gaps 2	
Qy	1 GPGTKKVVHVFYFKGKNVLNKIRCKDDSFTHLYTLIVRPNTYEVKIDNSQVSGSL 60 
Db	142 GFGTKKVVHVFYFKGKNVLNKIRCKDDSFTHLYTLIVRPNTYEVKIDNSQVSGSL 201 
Qy	61 DWDFELPPKKIKDPDAASKPEWDRAKIDDPDSKEDNDKPHIIPDPAKPEDWDEEM 120 
Db	202 DWDFELPPKKIKDPDAASKPEWDRAKIDDPDSKEDNDKPHIIPDPAKPEDWDEEM 261 
Qy	121 DGWEPPPVIQNPEYKGWKPKQIDNPDKGTWTWHPSIDNPEYSPDPSIYADNFVGLGD 180 
Db	262 DGWEFPPLIQNPEYKGWKPKQIDNPDKGTWTWHPSIDNPEYSPDPSNIYAVENFAVLGD 321 
Qy	181 LMQVKS GTTFNFLTINDEA VABFGNETWGVTAKAEKOMKDQDEOQLKEEEDKKRK 240 
Db	322 LMQVKS GTTFNFLTINDEA VABFGNETWGVTAKAEKOMKDQDEOQLHEEBEKKGK 381 
Qy	241 EEEEAEDKDEDDEDDEEDEED -VFGAKDEL 280
Db	382 EEEAAE-KDDDEDDEDDEDDEEBEEDSDAAAAGAKDEL 421

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RESULT 8
CRIC_DROME
ID _CRIC_DROME STANDARD; PRT; 406 AA.
AC P294I3; Q9VHA3;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Calreticulin precursor (CRP55) (Caeregulin) (HACBP).
CSC OR CG9429.
GN Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OC NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93208374; PubMed=1296819;
RA Smith M.J.;
RT "Nucleotide sequence of a Drosophila melanogaster gene encoding a
RT calreticulin homologue.";
RL DNA Seq. 3:247-250(1992).

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Query Match      63.8%; Score 991.5; DB 1; Length 395;
Best Local Similarity 66.0%; Pred. No. 1.5e-51;
Matches 173; Conservative 35; Mismatches 53; Indels 1; Gaps 1;

QY      1  GPGTKKHVIVNYKGNVLINKDIRCKDDFTHLVTLIVRPDNTVEVKIDNSQVESGSLE 60
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      134 GP-TARVHVILNYKGNKLIKKEITCKSDELTHVTLILNSDNTVEVLDGESAQTSLE 192

QY      61  DDWDELPPKTKIDPDASKPDWDERAKIIDPDTSKSDWDKDEHFPDPAKKPDWDEEM 120
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      193 EDWDLPPAKTKIDPDAKKPDWDEREYIDDAEDAKPEDWEKPEHFPDPAKKPDWDEEM 252

QY      121 DCEWEPPVIONPEYKGWPKQRQDNDPDYKGTWTHPEIDNPEYSPDPSIYAYDNFVLGLD 180
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      253 DCEWEPPMIDNPEYKGWPKQIKNPAYKGTWHPSEIENPEYTPDDELVSYESMCAIGFD 312

QY      181 LWQVKSGTIFNFNLTINDEAYAEFGNEITGWTKAAEKQMKQDQDEEOLKEEEDKKK 240
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      313 LWQVKSGTIFNIIITDSVEEAHAHAETPKDKVTKEKKEKADEETRKAEERKAAE 372

QY      241 EEEEAEDKDEDKDEDEEDEE 262
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      373 EEKAKKDDDEEKEEBEGHDE 394
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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DB	136	GFQTKVHVILPHYKDRRAHMHKDWLCKKDDVF	THLILLVNSDNIIEVQIDGERAKBSGGETE	139
QV	61	DDWDFEPKKIKDPDASKPEDWDERAKITDPT	TSKSPBWDKPEHIPDPDAKKPDPWDEEM	120

Db 196 ADWFLPPKKIKDPDAKPEDWDEREFDDDDKPKPEDDKPEHIDPDPAKPEDWDDDEM 255  
 QY 121 DGEWEPPIVIONPEYKGEWKPRQIDNDYKGTWHPIDNPEYSPDPSPSYAVDNFVGLGLD 180  
 Db 256 DGEWEPPIVIONPEYKGEWKPKQKPKAYKGIHPEIBIDYTPDNLYVDDIGALGFD 315  
 QY 181 LMQVKSCTTFDNLITNDEAYABBNQETWGTAAEKQMDKQDEEORLKEEBED---- 236  
 Db 316 LMQVKSCTTFDNLITNDEAYABBNQETWGTAAEKQMDKQDEEORLKEEBED---- 236  
 QY 237 --KGRKEEBEAEDK 248  
 Db 375 KMKRKRANRKKK 388

RESULT 11  
 CRIC RICO  
 ID CRIC RICO STANDARD; PRT; 415 AA.  
 AC P93508;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Calreticulin precursor.  
 OS Ricinus communis (Castor bean).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids I; Malpighiales; Euphorbiaceae; Acalyphoideae; Acalyphaeae;  
 OC Ricinus.  
 OX NCBI\_TaxID=3988;  
 RN [1]  
 RP MEDLINE=97435975; PubMed=9290642;  
 RA Coughlan S.J., Hastings C., Winfrey R. Jr.;  
 RT "Cloning and characterization of the calreticulin gene from Ricinus  
 communis L.";  
 RL Plant Mol. Biol. 34:897-911(1997).  
 CC -!- FUNCTION: This protein binds calcium. There are both high and low  
 affinity calcium-binding sites.  
 CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.  
 CC -!- SIMILARITY: Belongs to the calreticulin family.

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 -----  
 EMBL; U74631; AAB71420.1; -;  
 EMBL; U74630; AAB71419.1; -;  
 PIR; T10172; T10172.  
 DR InterPro; IPR009033; Calret calnex P.  
 DR InterPro; IPR001580; Calreticulin.  
 DR InterPro; IPR008985; ConA like\_rec\_gl.  
 DR InterPro; IPR000886; ER target S.  
 DR Pfam; PF00262; calreticulin; 1.  
 DR PIRSF; PIRSF002356; Calreticulin; 1.  
 DR PRINTS; PR00626; Calreticulin; 1.  
 DR PROSITE; PS00803; Calreticulin; 1.  
 DR PROSITE; PS00804; Calreticulin; 1.  
 DR PROSITE; PS00805; CALRETICULIN REPEAT; 2.  
 DR Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.  
 SIGNAL 1 20 POTENTIAL.  
 CHAIN 21 415 CALRETICULIN  
 FT CARBOHYD 52 52 N-LINKED (GLNAC. . .) (POTENTIAL).  
 FT CARBOHYD 152 152 N-LINKED (GLNAC. . .) (POTENTIAL).  
 FT SITE 412 415 PREVENT SECRETION FROM ER (POTENTIAL).  
 SEQUENCE 415 AA; 47522 MW; DDSP452E76CC7F8C CRG64;

Query Match 55.2%; Score 856.5; DB 1; Length 415;  
 Best Local Similarity 55.3%; Pred. No. 1.3e-43;  
 Matches 157; Conservative 36; Mismatches 80; Indels 11; Gaps 4;  
 QY 1 GPQTKKHVIFNYKGNVLKINDIRKDDFFHLYTLIVRPNTYEVKINDNSQVSGSL 60  
 Db 139 GYSTKKVHAFLNNDNHLIKKEVPCEVDQTLTVYTLVIRPDATYSLIDNVEKQTGSL 198  
 QY 61 DMDFLPPKKIKDPDAKPEDWDERAKIDDPDTSKPEDWK-PEHIPDPAKPEDWDEE 119  
 Db 199 TDWDLPPKKIKDPDAKPEDWDEKEIIPDPDKKEGDDIPKEIPDPAKPEDWDDDE 258  
 QY 120 MGEWEPPIVIONPEYKGEWKPRQIDNDYKGTWHPIDNPEYSPDPSPSYAVDNFVGLGL 179  
 Db 259 EDGEWTAPTIANPEYKGPWKPKKIKPNYKGNKAFMIDNPFKDDPEIYVYVPLKYVGI 318  
 QY 180 DLQVKSCTTFDNLITNDEAYABBNQETWGTAAEKQMDKQDEEORLKEEBEDKKR 239  
 Db 319 ELQVKSCTTFDNLITNDEAYABBNQETWGTAAEKQMDKQDEEORLKEEBEDKKR 239  
 QY 240 KBEAEAEKDE 375  
 Db 376 PADSDADEDDDDADDTEGDDGDSKSDAEDSAEDV---HDEL 415

RESULT 12  
 CRIC CHIRE  
 ID CRIC CHIRE STANDARD; PRT; 420 AA.  
 AC Q9STD3;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Calreticulin precursor.  
 OS Chlamydomonas reinhardtii.  
 OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;  
 OC Chlamydomonadaceae; Chlamydomonas.  
 OX NCBI\_TaxID=3055;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Zupplini A., Kaydamov C.;  
 RT "Cloning and characterization of a cDNA encoding Chlamydomonas  
 reinhardtii calreticulin.";  
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: This protein binds calcium. There are both high and low  
 affinity calcium-binding sites (by similarity).  
 CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By similarity).  
 CC -!- SIMILARITY: Belongs to the calreticulin family.  
 -----  
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 -----  
 EMBL; AJ000765; CAB54526.1; -;  
 DR InterPro; IPR009033; Calret calnex P.  
 DR InterPro; IPR001580; Calreticulin.  
 DR InterPro; IPR008985; ConA like\_rec\_gl.  
 DR InterPro; IPR000886; ER target S.  
 DR Pfam; PF00262; calreticulin; 1.  
 DR PIRSF; PIRSF002356; Calreticulin; 1.  
 DR PRINTS; PR00626; Calreticulin; 1.  
 DR PROSITE; PS00803; Calreticulin; 1.  
 DR PROSITE; PS00804; Calreticulin; 1.  
 DR PROSITE; PS00805; CALRETICULIN REPEAT; 1.  
 DR Endoplasmic reticulum; Calcium-binding; Repeat; Signal.  
 SIGNAL 1 18 POTENTIAL.  
 CHAIN 19 420 CALRETICULIN

FT SITE 417 420 PREVENT SECRETION FROM ER (POTENTIAL).  
 SQ SEQUENCE 420 AA; 47327 MW; DD3BA3AFFBF61C9B CRC64;

Query Match  
 Best Local Similarity 53.9%; Score 837.5; DB 1; Length 420;  
 Matches 154; Conservative 43; Mismatches 65; Indels 23; Gaps 4;

QY 1 GPGTKVHVFNKGVNKLNDIRCKDDEFHLYTLIVRPNTVEVKIDNSQVSGSLG 60  
 DB 141 GYSTRKVVHLYTKGKNLYLKDKIAETQDLTHVTVFIRPDATYSLIDNEKHGTGSIYEHM 200  
 QY 61 DMDLFPKKIKDPDASKPEDWDERAKIDDPDTSKPEDWDK-PEHIPDPDAKKPEDWDDE 119  
 DB 201 EDWMLPPKTIKPKASKPEDWDEREIAIDPEKKEGWDIDPATIADKDAKKPEDWDE 260  
 QY 120 MDEWEPVQNPPEYKGEWKPRQIDNPDKYGTWHPIDNPPEYSDPSIYAYDNFGLGL 179  
 DB 261 EDGTWEPMLPNPEYKGEWKPRQIDNPDKYGTWHPIDNPPEYSDPSIYAYDNFGLGL 320  
 QY 180 DLQVSGTIFDNFLITNDDEAYAEFGNETGWTKAAEKQMKDKQDEORLKEBEDKKR 239  
 DB 321 ELQVSGSIFDNFLITNDDEAYAEFGNETGWTKAAEKQMKDKQDEORLKEBEDKKR 374  
 QY 240 KE-----BEEAEKDDKDEDE-----EDEDKEDE 268  
 DB 375 KDAPPVPDAAEEDEVEDKEEPESGMGIKIPKEEESGHDE 419

RESULT 13  
 CRT2 MAIZE  
 ID CRT2 MAIZE STANDARD; PRT; 420 AA.  
 AC Q9SP2;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Calreticulin precursor.  
 GN CRT.  
 OS Zea mays (Maize).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC PACAD clade; Panicoideae; Andropogoneae; Zea.  
 OX NCBI\_TaxID=4577;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21862796; PubMed=11874098;  
 RA Wyatt S.E., Tsou P.-L., Robertson D.,  
 RT "Expression of the high capacity calcium-binding domain of  
 RT calreticulin increases bioavailable calcium stores in plants."  
 RL Transgenic Res. 11:11-10(2002).  
 CC -1- FUNCTION: This protein binds calcium. There are both high and low  
 CC affinity calcium-binding sites (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By similarity).  
 CC -1- SIMILARITY: Belongs to the calreticulin family.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch))  
 CC -----  
 CC EMBL: AF190454; AF014701.1; -; calnex.P.  
 DR InterPro: IPR009033; Calret. calnex.P.  
 DR InterPro: IPR001580; Calreticulin.  
 DR InterPro: IPR008985; ConA like lec\_gl.  
 DR InterPro: IPR000886; ER target S.  
 DR Pfam: PF00262; calreticulin; 1-  
 DR PRF: PRSF002356; Calreticulin; 1.  
 DR PRIN: PR00626; CALRETICULIN.  
 DR ProDom: PD001866; Calreticulin; 1.  
 DR PROSITE: PS00014; ER\_TARGET; 1.  
 DR PROSITE: PS00803; CALRETICULIN\_1; 1.

DR PROSITE; PS00804; CALRETICULIN\_2; FALSE NEG.  
 DR PROSITE; PS00805; CALRETICULIN\_REPEAT; 2.  
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.  
 FT SIGNAL 1 25 POTENTIAL.  
 FT CHAIN 26 420 CALRETICULIN.  
 FT CARBOHYD 57 57 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT SITE 417 420 PREVENT SECRETION FROM ER (POTENTIAL).  
 SQ SEQUENCE 420 AA; 47939 MW; E7387F43E7494735 CRC64;

Query Match  
 Best Local Similarity 53.9%; Score 837.5; DB 1; Length 420;  
 Matches 147; Conservative 49; Mismatches 77; Indels 5; Gaps 2;

QY 4 TKVHVHFNKGVNKLNDIRCKDDEFHLYTLIVRPNTVEVKIDNSQVSGSLEDW 63  
 DB 147 TKVHVHFNKGVNKLNDIRCKDDEFHLYTLIVRPNTVEVKIDNSQVSGSLEDW 206  
 QY 64 DFLPPKKIKDPDASKPEDWDERAKIDDPDTSKPEDWDK-PEHIPDPDAKKPEDWDEMDG 122  
 DB 207 DFLPPKKIKDPDASKPEDWDERAKIDDPDTSKPEDWDK-PEHIPDPDAKKPEDWDEMDG 266  
 QY 123 EWEPPVQNPPEYKGEWKPRQIDNPDKYGTWHPIDNPPEYSDPSIYAYDNFGLGLDW 182  
 DB 267 EWTAPTIPNPEYKGPWKQKIKNPNYQGWKAPMDINPDFKDDPYIYAFDSIKYIGELW 326  
 QY 183 QVKSGLTFDNFLITNDDEAYAEFGNETGWTKAAEKQMKDKQDEORLKEBEDKKRKEE 242  
 DB 327 QVKSGLTFDNFLITNDDEAYAEFGNETGWTKAAEKQMKDKQDEORLKEBEDKKRKEE 382  
 QY 243 ERAEDKDDKDE 280  
 DB 383 DE 420

RESULT 14  
 CRT2 ARATH  
 ID CRT2 ARATH STANDARD; PRT; 424 AA.  
 AC Q38858; O04152; O80486;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Calreticulin 2 precursor.  
 GN CRT2 OR CRTL OR ATIG09210 OR T12M4.8.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RX MEDLINE=21016719; PubMed=11130712;  
 RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,  
 RA White O., Alonso J., Altieri H., Araujo R., Bowman C.L., Brooks S.Y.,  
 RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,  
 RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,  
 RA Dunn P., Eggu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y.,  
 RA Gill J.E., Goldsmith A.D., Haas B., Hansen M.F., Hughes B., Huizar L.,  
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,  
 RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,  
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,  
 RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,  
 RA Miliuteer J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,  
 RA Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,  
 RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,  
 RA Sun H., Taiton L.J., Tambunga G., Toriumi M.J., Town C.D.,  
 RA Uterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,  
 RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;  
 RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis  
 thaliana."  
 RL Nature 408:916-920(2000).  
 RN [2]  
 RP SEQUENCE OF 1-174 FROM N.A.



QY 120 MDGEWEPVIONPEYKGEWKPKQIDNPDYKGTWIIHPEIDNPEYSPDPSIYAYDNFVGL 179  
Db 263 EDGEWTAPTIPNPEYKGEWKPKKIKPNPKGKWKAPLIDNPEFKDDPELYVYPNLKYVG 322  
QY 180 DLQVKSGTIFDNFLITNDAYAEFFGNETGVTKAAEKQMKDKQDEBQRLKEEEDKXR 239  
Db 323 ELQVKSGLFDNLIITDEPEYAKQLABETWKGQKDAKA---AFEELEKQLQEEESKED 379  
QY 240 KEEEAEDKEDDE 280  
Db 380 PVDSDAED-DDNEAEDGEESDSEKPDSTESAEATEAKHDEL 421

Search completed: October 12, 2004, 15:46:32  
Job time : 14 secs

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